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4.5	Compugen
á	- 2000
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

June 20, 2001, 12:07:40 ; Search time 13.02 Seconds (without alignments) 1470.723 Million cell updates/sec Run on:

US-09-425-501-2
2981
1 MPLVKRNIDPRHLCHTALPR.....AVEYSDSEDDSEFDEVDWLE 559 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 al number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	092558 homo sapien	4 mus	SILE	hom	P13983 nicotiana t	r.	Q03211 nicotiana t	_	043516 homo sapien	_	P42768 homo sapien	~			Q05860 mus musculu			-				zea m	daucus ca	P40602 arabidopsis		P54258 rattus norv	Q12446 saccharomyc	Q03209 autographa	Q15427 homo sapien	P24152 sorghum bic	010341 orgyia pseu	homo sa	
SUMMARIES		a	Y269_HUMAN	FMN2_MOUSE	DIAL MOUSE	DIA1_HUMAN	EXTN_TOBAC	WASP_MOUSE	EXLP_TOBAC	FM14_MOUSE	WAIP_HUMAN	SP62_MOUSE	WASP_HUMAN	EBN2_EBV	CAPU_DROME	SSGP_VOLCA	FMN1_MOUSE	MUC2_HUMAN	PRF1_LYCES	FMN_CHICK	VRP1_YEAST	TRX2_HUMAN	SP62_HUMAN	EXTN_MAIZE	EXTN_DAUCA	APG_ARATH	SEPA_EMENI	DRPL_RAT	LA17_YEAST		SP49_HUMAN	EXTN_SORBI	Y091_NPVOP	DRPL_HUMAN	TEGU_EBV
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	YK82_MYCTU	PRP2 MOUSE	VP61_NPVOP	MNT_HUMAN	Y091_NPVAC	YAV1_SCHPO	PRP3_MOUSE	TEGU_HSVEB	T2D3_HUMAN	SFPO_HUMAN	SRA4_RAT	TEGU_HSV11	
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	245.5	243.5	243.5	243	242.5	242	241	238.5	237.5	236	235	235	
	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Y269_ ID ID	TY269_HUMAN	STANDARD;	PRT;	559 AA	i			
1223	(Rel.		ed)	update)				
E E E	01-NOV-1997 (Rel. 3 HYPOTHETICAL PROLIN KIAA0269	Last NICH P	annotation updat ROTEIN KIAA0269.	n updat AA0269	(e)			
SOS	Homo sapiens (Human)	$\overline{}$:	•		•	
38	Mammalia; Eutheria;	; Chordata; ; Primates;		ra; ver iini; P	Craniata; Vertebrata; Catarrhini; Hominidae;	; Euteleostomi e; Homo.	stom1;	
X OX	NCBI_TaxID=9606;							
RP.	SEQUENCE FROM N.A.							
% % %	TISSUE-Bone marrow; MEDLINE-97191544; PubMed-9039502;	; PubMed≖9039	502:					
RA.	Nagase T., Seki N.,	N., Ishikawa	KI.,	Ohira M.,	í., Kawa	Kawarabayasi	Υ.,	
R K	Unara O., Tanaka A. "Prediction of the	Tanaka A., Kotani H., Miyajima N., Nomura on of the coding sequences of unidentified	I., Miya mences	jima N. Jima N.	, Nomur Pentifie	N.; himan	J. Souds	. 10
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0	es of 80 ne	w genes	(KIAA	(KIAA0201-KIAA0280)	1280)	٠.	 by
RT	analysis of cDNA cl	lones from	cell lir	ne KG-1	and brain."	ain.";)
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မ		non-profit institutions as long	lons as	long	ro	is its content is in no way	is in	000
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		333	POLY-PRO.					
		3.56	POLY - PRO					
FT	DOMAIN 369	374	POLY - PRO.					
		435	POLY-PRO					
ÖS.	SEQUENCE 559 AA;	61652 MW;		44B4527BDB77BC6E		CRC64;		
Ouc	Query Match Best Local Similarity	100.08;		2981;	DB 1;	Length 55	, (6)	
Mat	Matches 559; Conservative	rative 0	4	. 01		Indels	o; Ga	Gaps
οy	1 MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEAH	HTALPRGIKN	ELECVTNI	SLANII	ROLSSLS	KYAEDIFGE	LFNEAH	09
QQ	1 MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEAH	CHTALPRGIKN	ELECVIN	SLANII	RQLSSLS	KYAEDIFGE	LFNEAH	09
οy	61 SFSFRVNSLOERVDRLSVSVTQLDPKEEELSLQDITWRKAFRSSTIQDQQLFDRKTLPIP	RLSVSVTQLD	PKEEELSI	ODITME	KAFRSST	IODOOLFDR	KTLPIP	120
	61 SFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITWRKAFRSSTIODOOLFDRKTLPIP)	PKEEELSI	ODITMR	KAFRSST	IODOOLFDR	KTLPIP	120
							;	,

121 LQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKQK 180

δ

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Atd.
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OM nucleic - nucleic search, using sw model

Run on:

June 20, 2001, 15:04:28; Search time 3470.44 Seconds

(without alignments)

11699.624 Million cell updates/sec

Title:
Perfect score: 2625
Sequence:
1 cttctttgcacttgcggat.....aatggttcattttaaaagtt 2625
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0
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il number of hits satisfying chosen parameters: 2688314

1344157 seqs, 7733874588 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

83: 9b_htg24:*
84: 9b_htg24:*
85: 9b_htg25:*
86: 9b_pr2:*
87: 9b_pr3:*
89: 9b_pr4:*
89: 9b_pr6:*
91: 9b_pr6:*
92: 9b_pr6:*
93: 9b_pr6:*
94: 9b_pr6:*
95: 9b_r01:*
95: 9b_r02:*
96: 9b_pr01:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

em_htg_inv2

em_in:* em_om:* em_or:*

No. Score Match Length DB ID Description 1 2625		1	مبر سیکار،	ä	-	. 7	4.7	1.7	1.7	. -	•
Score Match Length DB ID 2625 (100.0) 2625 91 DB7459 1782.6 67.9 2469 94 AF290877 1758 67.0 1758 9 AF230877 861.4 32.8 151580 82 AE590009 861.4 31.9 213475 87 AC019100 751.2 28.6 143812 66 AC021847 282.6 10.8 1509 85 AB026543		_	lan mKN	fus musc	lomo sar	1000	Tomo of			Tes Ollo	350
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89 AF134305 85 AB020707 66 AC021847 91 AP000508 91 AP000508
85 AC004204 86 AC007263 5 AF247764 4 AC007186 4 AC073495 86 AC017042 86 AC017042 80 AC017042 81 AC07821 82 AC000097 85 AC006549 86 AC006549 86 AC006549 86 AC006549 86 AC006549 86 AC006549
Homo Homo Arabi Arabi Homo Homo
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D87459 2625 bp mRNA PRI 10-JUL-1997 QY HUMAN mRNA for KIAA0269 gene, complete cds. D87459 D87459 G G G G G G G G G G G G G G G G G G G
Monto septens male brain cDNA to mRNA, clone_lib:pSPORT 1 clone:HA6751. Homo saplens Bukartayota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; QY Ammalla: Buthbaria: Drimates: Catarrhiot: ucminidas. ucm

Nagase,T., Seki,N., Ishikawa,K. and Nomura,N.
Prediction of the coding sequences of unidentified human genes.VI.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of CDNA clones from human cell line KG-1 and brain Unpublished (1996) Direct Submission

Direct Submission

Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo Nomura, Kazusa DNA Research Institute, Gene Structure 1; 1532-3 Yana, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931) Primates; Catarrhini; Hominidae; Homo Mammalia; Eutheria; 1 1 (bases 1 to 2625)

> REFERENCE AUTHORS TITLE JOURNAL

Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y., Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain

(sites)

REFERENCE AUTHORS

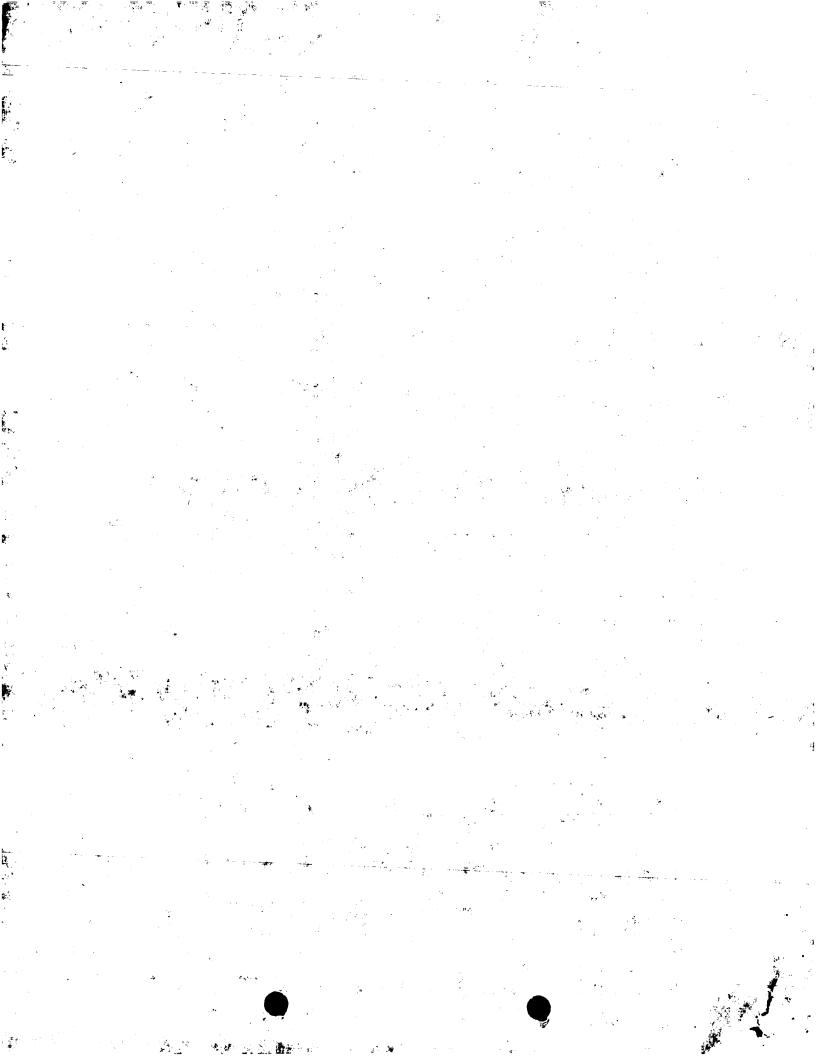
TITLE

JOURNAL

AUTHORS TITLE

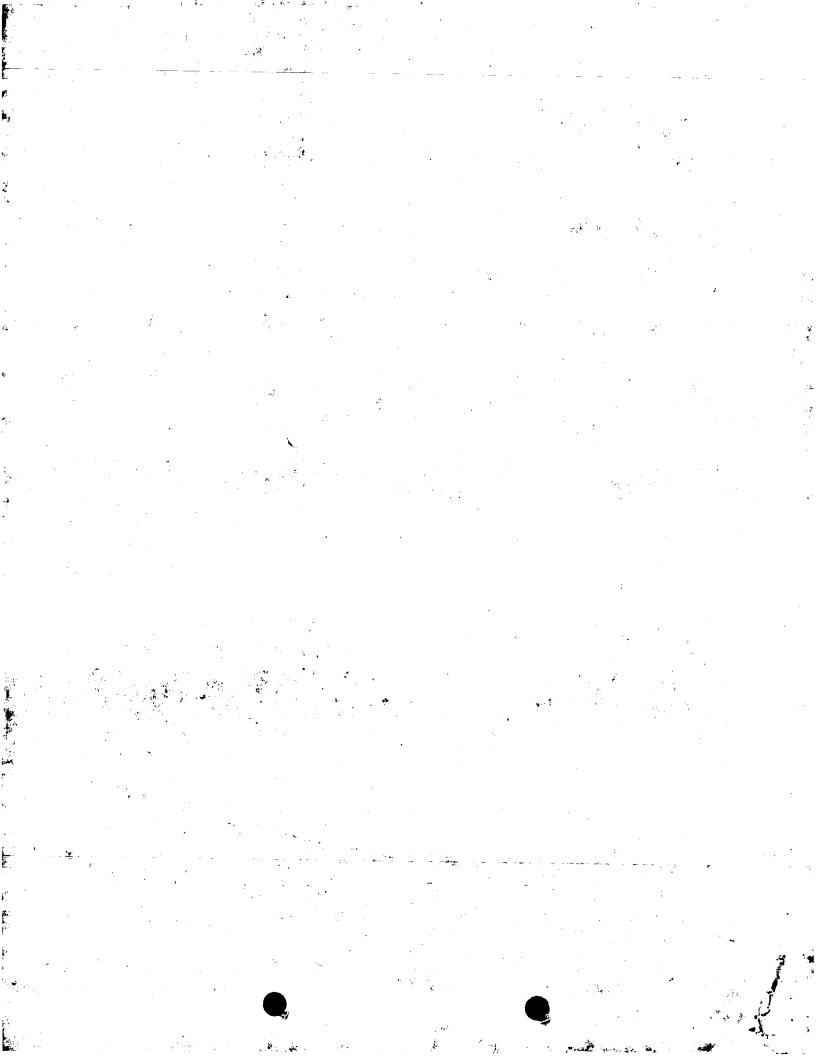
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IPPPPPMHGAGDAKPIPTCISSATGILENRPQSPATGRTPVYSPTPPPPPPPPPLPSA
STSSILRASMYSTPPPPPPPPPPPATALQAPAVPPPPAPLQIAVGVLHPARPPIAPP
VQPSPPVARAAYUCETVPVHPLPQGSVQGLPPPPPPPPPPPPPPPGIRPSSPVTVTALAH
PSGLHPTPSTAGPHYPLMPSSPSQVIPASERKRHPSTLPVISDARSVLLEAIRKG
QLRKVVEQNPARAHENILSRRIAVETILSRRIAVEYSDSEDDSEFDEVDWLE"
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(YAEDIFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFR
STIQDQQLFDRKTLPIPLQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDL
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                                                                                                                       clone_lib="pSPORT 1"
sex="male"
(5), 321-329 (1996)
                                                                                                                                                          .type="brain"
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                                   ocation/Qualifiers
                                                                                                                                                                                              gene="KIAA0269"
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541 CTTTCCG				CTACT
601 cattace 601 CATTACA	cattacaggagacgtacgatgtttgtgaacagcctccacctctcaatatactcactc		Qy 1681 Db 1681	ctgctt CTGCTI
661 atagag 661 ATAGAG	ttgatc 7 rrgarc 7		Qy 1741 Db 1741	tgctac TGCTAC
21 tatgg 21 TATGG			Qy 1801 Db 1801	aggaag AGGAAG
81 agcag 81 AGCAG	ω ω	·	Qy 1861 Db 1861	ctgttg CTGTTG
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1021 tgagt 1021 TGAG7	108		Oy 2101 Db 2101	tttaca TTTACA
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1141 ctac 1141 CTAC	m — m		Qy 2221 Db 2221	attgtg
1201 tgag 201 TGAG	tgagcccactccccactcctccaccactcttccatctgccttgtcaacttcctcat 1260 		Qy 2281 Db 2281	gctgta GCTGTA
1261 taag 261 TAAG	taagagetteaatgaetteaaeteeteeeeteeagtaeeteeeeeaeeteeag 1320 		Qy 2341 Db 2341	ttgatt TTGATT
1321 ccac 1321 CCAC	n - n		Oy 2401 Db 2401	gaatgc GAATGC
1381 gagt 1381 GAGT		<u>.</u>	Oy 2461 Db 2461	tttagc TTTAGC
1441 taget 441 TAGET			Qy 2521 Db 2521	gttaaa GTTAAA
1501 ttcag 501 TTCAG	tcaggggotgoctcoaccocaccaccaccactcttgctccacctggattcgaccat 1560 	<u> </u>	Oy 2581 Db 2581	ttaaga TTAAGA
1561 catca 561 CATCA	catcacctgtcacagttacagctcttgctcatcctccctc		RESULT 2 AF290877 LOCUS	
1621 ctact	ctactgccccaggtccccatgttccattaatgcctccatcca		DEFINITION ACCESSION VERSION	Mus AF29 AF29

1860 1980 2100 2100 2160 2160 2280 2340 2340 2400 2400 2460 2460 GCCCCAGGTCCCCATGTTCCATTAATGCCTCCATCTCCTCCATCACAAGTTATAC 1680 2580 10-0CT-2000 tatacgaatacactcagaaagtacatttagcttgtagtgttgaattctcttaaag gtactttgtgaattttaatttaaagaaagcaactgaaattgaaatcttgagggca ROD 190877 2469 bp mRNA musculus WAVE-1 mRNA, complete cds. AF290877.1 GI:9931545



GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

protein search, using sw model

June 20, 2001, 12:07:40 ; Search time 13.02 Seconds

(without alignments) 1470.723 Million cell updates/sec

US-09-425-501-2

.... AVEYSDSEDDSEFDEVDWLE 559 1 MPLVKRNIDPRHLCHTALPR..... sednence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

93435 segs, 34255486 residues searched:

number of hits satisfying chosen parameters:

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prinand is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			٠.		
No.	Score	Match	Length	80	 1		Description
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•	T067	7	י מי	٠.	I ZOS HUMAN		
	334	11.2	1567	٦	FMN2_MOUSE	-	O91104 mus musculu
m	-	10.7	1255	-	DIA1_MOUSE		008808 mus musculu
4	313.5	10.5	1248	-	DIAL HUMAN	•	рошон
'n	309	10.4	, 620	-	EXTN TOBAC	-	nicot
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7	286.5	9.6	426	-	EXLP TOBAC		200
8	286.5	9 6	1206	-			6
6	284	 6	503	ر آ	WAIP_HUMAN		homo
9	281	4.6	485	-	SP62_MOUSE	-	3 mus m
	280	9.4	502	Н	WASP_HUMAN		homod
53	275.5	9.5	487	П.	EBN2_EBV		epste
13	275	9.5	1059	H	CAPU_DROME		
14	273:5	9.5	485	-	SSGP_VOLCA		
15	272.5	9.1	1468	-	FMN1_MOUSE		
16	270.5		5179	-	MUC2_HUMAN		Q02817 homo sapien
17	269.5	0.6	346	-	PRF1_LYCES		_
18	269.5	0.6	1213	-	FMN_CHICK		m
19	268.5	0.6	817	-	VRP1_YEAST	•) sacchar
20	267.5	0.6	2715	-	TRX2_HUMAN	•	Q9umn6 homo sapien
21	ω.	6. 6.	464	-	SP62_HUMAN		3 homo
22	263	œ.	- 267	-	EXTN_MAIZE		3 zea m
23	259.5	8.7	306	Ä	EXTN_DAUCA		_
77	257.5	8	534	~			Ċ
25	256	8	1790	÷	SEPA_EMENI		P78621 emericella
56	253.5	8	1183	Ä	DRPL_RAT		P54258 rattus norv
27		80	633		LA17_YEAST		Q12446 saccharomyc
83		4.	543	-	VP61_NPVAC	-	003209 autographa
50	248.5	e. 9	424	-	SP49_HUMAN		27
) T	248	m (283	Н,	1	-	52 sorgh
5 00	247	Φ	279	- -	~ 1		덬
7	246.5	œ	1185	H	DRPL_HUMAN	· · ·	29
(C)	246.5	8.3	3149	-	TEGU_EBV		P03186 epstein-bar

61 SFSFRVNSLORDVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQLFDRKTLPIP 120 61 SFSFRVNSLQERVDRLSVSVTQLDPKEBELSLQDJTMRKAFRSSTJQDQQLFDRKTLPIP 120 121 LOETYDVCEOPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLODTEDKRKEKRKOK "180"

1 MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEÄH 60

100.0%; Score 2981; DB 1; Length 559; llarity 100.0%; Pred. No. 1.5e-133; Conservative 0; Mismatches

Similarity

Matches 559; Query Match

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Q10690 mycobacter1	PO5142 mus musculu	O10270 orgyta pseu	099583 homo sapien	P41479 autographa	Q10172. schizosacch	PO5143 mus musculu	P28955 equine herp	000268 homo sapten,	P23246 homo sapten	Q63627 rattus norv	P10220 herpes simp	
				-						-		
YK82_MYCTU	PRP2_MOUSE	VP61_NPVOP	MNT_HUMAN	Y091_NPVAC	YAV1_SCHPO	PRP3_MOUSE	TEGU_HSVEB	T2D3_HUMAN	SFPO_HUMAN	SRA4_RAT	TEGU_HSV11	
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721	261	474	582	224	1794	296	3421	1083	707	1048	3164	
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ALIGNMENTS

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	559 AA:	odate)	update)		:	Vertebrata; 1; Hominidae;			•	Ohira M., Kawarabayasi	z	sequences of unidentified huma	* KG-1 and brain.			t is produced t	formatics and	There are	æ	See							44B4527BDB77BC6E CRC64;
	PRT;	Created) Last sequence update)	ء بد			Chordata; Craniata; V Primates; Catarrhini;			7; DibMed=9039502.		Kotani H., Miyajima N.,	sequences of			GANS RUCCE.B.	entry is copyright. I	Institute of Bioinformatics	bioiniormatics institute. T profit institutions as long		license agreement (See			Odd-v10d	BOLY-PRO.	POLY-PRO	POLY - PRO	MM;
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DR EMBL; AF218940; AAF72883.1; DR MGD; MGI:1859252; Fmn2.	InterPro; IPR001265; InterPro; IPR003104; Pfam; PF02181; FH2; 1. PRINTS; PR00828; FORMIN	KW Developmental protein; Repeat; FT DOMAIN 643 683 CO CO FT DOMAIN 735 1113 FH FT DOMAIN 919 1039 11	REPEAT 919 929 REPEAT 930 940 REPEAT 941 951	REPEAT 952 962 REPEAT 963 973 REPEAT 974 984 REPEAT 985 995	REPEAT 996 REPEAT 1007 REPEAT 1018 REPEAT 1029	DOMAIN 1128 1532 DOMAIN 1408 1444 DOMAIN 48 55 DOMAIN 202 207	DOMAIN 797 801 DOMAIN 797 801 DOMAIN 861 864 DOMAIN 908 917 DOMAIN 922 928	933 939 944 950 955 961 966 972 977	DOMAIN 988 994 DOMAIN 999 1005 DOMAIN 1010 1016 DOMAIN 1021 1027	FT DOMAIN 1032 1038 PO FT DOMAIN 1043 1046 PO FT DOMAIN 1054 1060 PO FT DOMAIN 1065 1072 PO FT DOMAIN 1065 1072 PO FT SEQUENCE 1567 A1: 166268 PW:	Query Match 11.2%; Best Local Similarity 26.7%; Matches 146; Conservative 5	LQDITMRKAFRSSTIQ- : : : : PKDVDTEPKSSILES	Oy 126 -DVCEQPPPLNILTPYRDDGKE-GLKI :: :: Db 668 AFLEKYVDAALDIEGPPGISCIENGIE	184	Qy 238 RPQTYVDHMDGSYSLSALPFSQMSEL	QY 279MHC	Db 829 SSSFGNNCNVPPAPPLETSSSFMP QY 314 GRIPVEVSPTPPPPPPPLR
DD 121 LOSTYDVCEOPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKOK 180	QY 181 QKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQ 240	QY 241 TYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPPMGAGDAKPIPTCISSA 300 1111111111111111111111111111111111	Oy 301 TGLIENRPOSPATGRIPVFVSPTPPPPPPLPSALSTSSLRASMISTPPPPPPPPPA 360 	Oy 361 TALQAPAVPPPPAPIQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEV 420 	Qy 421 QGLPPPPPPPPPPPPPRGSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPFSPPSQVIP 480	OY 481 ASEPKRHPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQEAKHERIENDVATILSRRIA 540 DD 481 ASEPKRHPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQEAKHERIENDVATILSRRIA 540		RESULT 2 FWN2_MOUSE ID FWN2_MOUSE STANDARD; PRT; 1567 AA.	O9JI04; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence updat 01-OCT-2000 (Rel. 40, Last annotation upd FORMIN 2.	GN FMN2. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.	TISSUE-Brain; MEDLINE-20245324; Pubmed-10781961; pader B., Leder P;	Subfamily, is highly expressed in the developing and adult onervous system. ; Allow the developing and adult onervous system. ; Allow and adult onervous system. ; TISSIE SPETITION.	•	+ + +	This SWISS-PROT entry is copyright. It is produced through a change the contract of the contra	the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its content.	modified and this statement is not removentities requires a license agreement (§ or send an email to license@isb-sib.ch).

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mRNA gene, complet mRNA for KIAA0269 2625 bp D87459.1 GI:1665804 **KIAA0269** 7459. D87459 EFINITION

Vertebrata; Euteleostomi; to mRNA, clone_lib:pSPORT 1 Homo sapiens male brain cDNA clone: HA6751: Homo saptens S

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E Mammalia, Eutheria, Primates, Catarrhini, Hominidae, 11. (bases 1 to 2625)

Submission

TITLE REFERENCE AUTHORS

REFERENCE

TITLE

Submitted (27, AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo Nomura, Kazusa. DNA Research Institute, Gene Structure 1, 1532-3 Yana! Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931)

of the coding sequences of unidentified human genes VI. sequences of 80 new genes (KIRA0201-KIRA0280) deduced t cona clones from human cell line KG-1 and brain Seki, N., Ishikawa, K. and Nomura, N. coding Nagase, T. Predictio

Unpublished (1996) (sites)

REFERENCE AUTHORS

TITLE

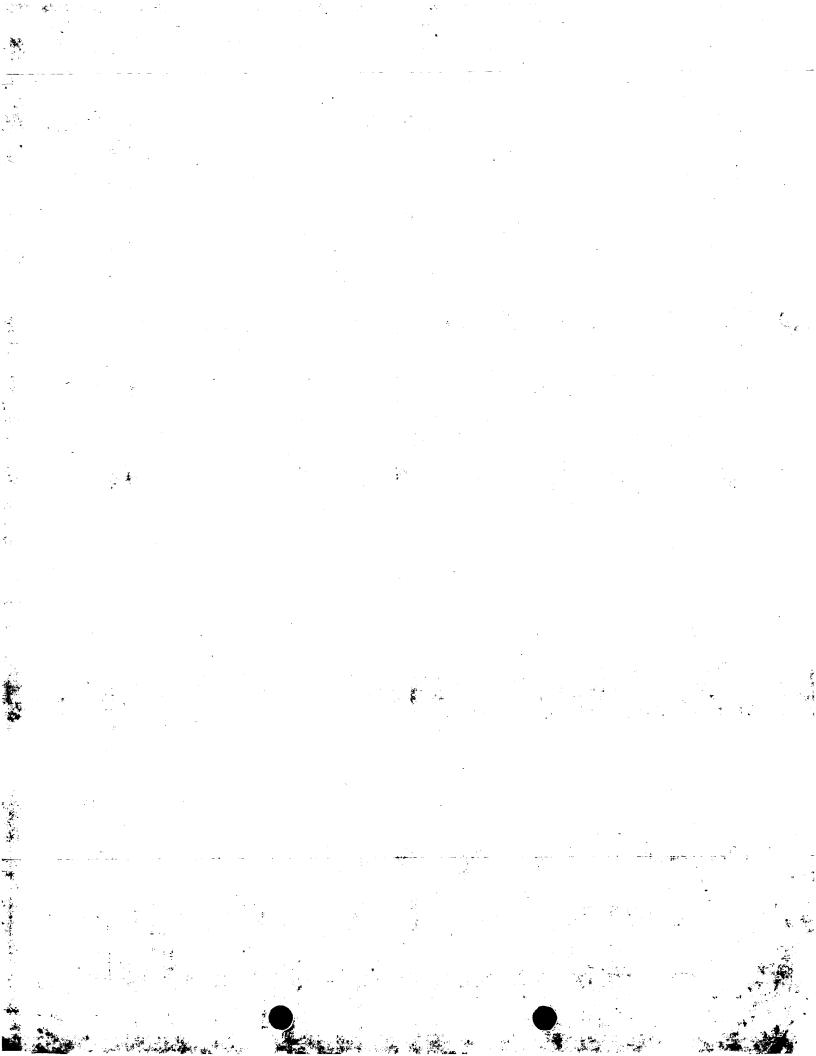
JOURNAL

of cDNA clones

analysis

Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y., Ohara, Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by from cell line analysis of

EPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPSA SSTIODQQLFDRKTLPIPLQETYDVCEQPPFLNILTPYRDDGKEGLKFYTNPSYFFDL WKEKMLQDTEDKRKEKRKQKQKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDA· NLLHKHIEVANGPASHFETRPQTYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPH LSTSSLRASMTSTPPPPVPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPP LVOPSPPARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSSPVTVTALAH /translation="MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSL PPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVLLEAIRKG SKYAEDIFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFR cttccgaagttctacaattcaagaccagcagcttttcgatcgcaagactttgcctattc 600 AACTAAGTAGCCTAAGTAAATATGCTGAAGATATTTTGGAGAATTATTCAATGAAGCAC 420 421 atagtttttccttcagagtcaactcattgcaagaacgtgtggaccgtttatctgttagtgy480 481 TTACACAGCTTGATCCAAAGGAAGAATTGTCTTTGCAAGATATAACAATGAGGAAAG 1540 agatgoogotagtgaaaagaaacatogatootaggoacttgtgooacacacagoactgoota 300 421 ATAGUTTTTCCTTCAGAGTCAACTCATTGCAAGAACGTGTGGACCGTTTATCTGTTAGTG '480 ggagaaatcagcatgttaaaacaactgttgatgatagctgttggagtaaagttgcagtgg 180 GGAGAAATCAGCATGTTAAAACAACTGTTGATGATAGCTGTTGGAGTAAAGTTGCAGTGG 180 0; Gaps DEVDWLE /note="Similar to Volbox carteri extensin (S22697)" /codon_start=1 DB 91; Length 2625; ttacacagettgatecaaaggaagaattgtetttgcaagatataacaatgaggaaag teaegtectgecetataacegattaattaattgateeceagetagaetagtgtt aagetatggetgeaaaategttaaaatetteaaggtgaaetggeacaaaggttaatetea gaggcattaagaatgaactggaatgtgtaaccaatatttccttggcaaatataattagac GAGGCATTAAGAATGAACTGGAATGTGTAACCAATATTTCCTTGGCAAATATTAGAC. 181 AAGCTATGGCTGCAAAATCGTTAAAATCTTCAAGGTGAACTGGCACAAAGGTTAATCTCA a a cta a gta g c cta a gta a a ta t g c t g a a g a ta t t t g g a a a t t a t t ca a t g a a g c a c **IQLRKVEEQREQEAKHERIENDVATILSRRIAVEYSDSEDDSEF** 0; Indels Score 2625; Pred. No. 0;); Mismatches /protein_id="BAA13399.1" /organism="Homo saplens /db_xref="taxon:9606" /clone="HA6751" /clone_lib="pSPORT 1" /sex="male" /tissue_type="brain" 243. .1922 /gene="KIAA0269" Location/Qualifiers 1. .2625 243. .1922 /gene="KIAA0269" CAACATTCACGTCCTGCCCTATAACCG ö 100.0%; C 809 Conservative Similarity Ouery Match Best Local Simil Matches 2625; C caacatt source COUNT 301 361 JOURNAL 361 gene 301 61 FEATURES CDS ā 셤 g δ 셤 à ð 윰 à ò



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TGLIENRPQSPATGRIPVFVSPIPPPPPPPLPSALSISSLRASMISTPPPPVPPPPPPA 360		FT	REPEAT	941
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		FT	REPEAT	974
TALGAPAVEPERAPLGIAFGVLHFAPPFIAFPLVQPSPFVARAAFVCETVFVHFLFQGEV 420		 E4 (REPEAT	985
		H.	REPEAT	966
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VEYSDSEDDSEFDEVDWLE 559		F	DOMAIN	861
		FT	DOMAIN	806
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		FT	DOMAIN	955
		FT	DOMAIN	996
MOUSE STANDARD; PRI; 1567 AA.	•	FI	DOMAIN	977
		FT	DOMAIN	988
(Rel. 40,	-	FJ	DOMAIN	666
(Rel. 40, Last	-	FT		1010
CT-2000 (Rel. 40, Last annotation update)		FI		1021
	•	FT		1032
	-	FT		1043
		FT	DOMAIN	1054
; Metazoa; Chordata;	- ,	FI	DOMAIN	1065
alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		FT		1077
TaxID=10090;		SO	SEQUENCE	1567' 1

11.2%; Score 334; DB 1; Length 1567; 26.7%; Pred. No. 5e-09; Live 53; Mismatches 184; Indels 164; Gaps 28; 87 EEELSLQDITMRKAFRSSTIQ-----10QQLFDRK----TLPIPLQETY----1155 126 -DVCEQPPPLNILTPYRDDGKE-GLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKGKQKN 183 610 EEEPSPKDVDTEP--KSSILESPKKCSNGVQQEVFDVKSEGQATVIQQLEQTIEDLRTKI 667 668 AELEKOYPALDLEGPRGLSGLENGLTASADVSLDALVLHGKVAQ------PPRTLEAKS 720 771 EISLIVSPRRISVQLDAQQIQSASQLPPPPPLLGSDSQ--GQPSQPSLHTESETSHEHSV 828 LD-RPHEPEKV----PRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFET 23 829 SSSFGNNCNVPPAPPLPCTESSSFWPGLGMAIPPPPCLSDITVPALPSPTAPALGESNLC 888 238 RPQTYVDHMDGSYSLSALPFSQMSEL----LTRAEERVLVRPHEP------Best Local Similarity 26.7% Matches 146; Conservative Query Match 184 ò à 셤

> It is produced through a collaboration (See http://www.isb-sib.ch/announce, his SWISS-PROT entry is copyright

1. Dev. 93:221-231(2000).
TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN THE DEVELOPING
AND MATURE CENTRAL NERVOUS SYSTEM:

AL AND ADDIT BRAIN STRUCTURES INCLUDING THE OLFACTORY BULB

NLAMUS HYPOTHALAMUS, HIPPOCAMPUS AND CEREBELLUM.
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DEVELOPMENTAL STAGE: EXPRESSION BEGINS AT EMBRYONIC DAY 9. 5 1 THE DEVELOPING SPINAL CORD AND BRAIN STRUCTURES AND CONTINUES

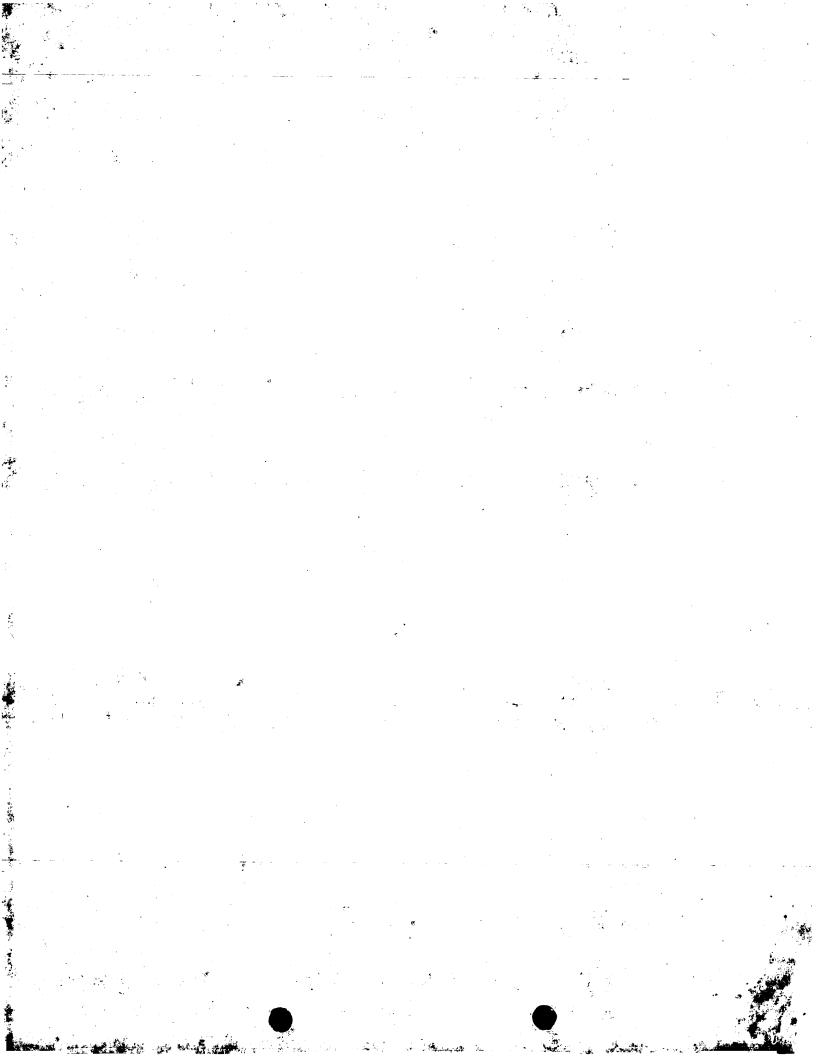
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---PPPPPLPSALSTSSLRASMTSTPPPP----VPPPPP----GRIPVEVSPIPP



homo sapien

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rattus norv herpes simp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-97191544; PubMed-9039502;
Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
Prediction of the coding sequences of unidentified human genes.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-I and brain.";
DNA Res. 3:221-329(1996).
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Y091_NPVAC
YAV1_SCHPO
PRP3_MOUSE
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T2D3_HUMAN
SFPQ_HUMAN
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-I TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN THE DEVELOPING AND MATURE CENTRAL NERVOUS SYSTEM.

-I DEVELOPMENTAL STRAGE: EXPRESSION BEGINS AT EMBRYONIC DAY 9. 5 IN THE DEVELOPING SPINAL CORD AND BRAIN STRUCTURES AND CONTINUES IN NEONATAL AND ADUIT BRAIN STRUCTURES INCLUDING THE OLFACTORY BULB, CORTEX, THALAMUS, HYPOTAMPUS, HIPPOCAMPUS AND CEREBELLUM.
-I SIMILARITY: CONTAINS I FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-I SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY 2 (FH2) DOMAIN.
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                                                 TYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPPMHGAGDAKPIPTCISSA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-20245324; PubMed-10781961;
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01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
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FH1 (PRO-RICH).
11 X 11 AA TANDEM REPEATS OF [MV]-G-I-P-P-P-P-L-P-G.
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3; Mismatches 184; Indels 164; Gaps
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                                                                                                                                                                                                                                                                                                                                                          COIL (POTENTIAL).
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Best Local Similarity 26.7'
Matches 146; Conservative
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MGD; MGI:1859252; Fmn2.
InterPro; IPR001265; -.
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                               InterPro; IPR003104; -
Pfam; PF02181; FH2; 1.
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-1-DOMAIN: DRFS ARE REGULATED BY INTRAMOLECULAR GBD-DAD BINDING WHERE RHO-GTP ACTIVATES THE DRFS BY DISSUPTING THE GBD-DAD INTERACTION.
-1-SIMILARITY: CONTAINS 1 GTPASS-BINDING DOMAIN (GBD).
-1-SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-1-SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-1-SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 3 (FH3) DOMAIN.
-1-SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 3 (FH3) DOMAIN.
-1-SIMILARITY: CONTAINS 1 DRF AUTOREGULATORY DOMAIN (DAD).
-1-SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. DIAPHANOUS
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MOL. Cell 5:13-25(2000).

- Cell 5:13-25(2000).

- FUNCTION: BINDS TO GTP-BOUND FORM OF RHO AND TO PROFILIN. ACTS IN

- FUNCTION: BINDS TO GTP-BOUND FORM OF RHO AND THE MEMBRANE, WHERE

IT PROMOTES ACTIN POLYMERIZATION. IT IS REQUIRED FOR CYTOKINESIS,

STRESS FIBER FORMATION, AND TRANSCRIPTIONAL ACTIVATION OF THE

SERUM RESPONSE FACTOR. DFR PROFILINS COUPLER RHO AND SRC TYROSINE

KINASE DUBING SIGNALING AND THE REGULATION OF ACTIN DYNAMICS.

- SUBCELLULAR LOCATION: MEMBRANE RUFFLES, ESPECIALLY AT THE TIP OF

RUFFLES, OF MOTHLE CELLS.
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889 GPEMLPAPPQPPPLPGLGVPPPPPAPPL-----PGMGIPPPPPLPGMGIPPPPPLPGM 941
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                                                  PQGEVQGLPPP----SGLHPTPSTAP
                                                                                                                                                       GPHVPLMPP-----PSTLPVISDARSVLL
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15-JUL-1999 (Rel. 38, Last sequence update)
01-CCT-2000 (Rel. 40, Last amoutation update)
DIAPHANOUS PROTEIN HOMOLOG 1 (DIAPHANOUS-RELATED FORMIN 1) (DRF1)
                             --PPATALQAPAVPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20142655; PubMed-10678165;
Tominaga T., Sahai E., Chardin P., McCormick F., Courtneidge
Alberts A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-97357293; PubMed-9214622;
Watanabe N., Madaule P., Raid T., Ishizaki T., Watanabe G.,
Watzuka A., Saito Y., Nakao K., Jockusch B.M., Narumiya S.;
"pl40mDia, a mammalian homolog of Drosophila diaphanous, is a
protein for Rho small GTPase and is a ligand for profilin.";
EMBO J. 16:3044-3056(1997).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
DIAPHANOUS PROTEIN HOMOLOG 1 (DIAPHANOUS-RELATED FORMIN 1) (DRF1).
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W; 09404164873CA7C1 CRC64;
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FH2.
COILED COIL (POTENTIAL)
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es 192;
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                      or send an email to license@isb-sib.ch).
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24.2%;
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InterPro; IPR003104; -
Pfam; PF02181; FH2; 1.
Coiled coil; Repeat.
DOMAIN 460 562
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Matches 138; Conserv
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                                                                                                                                                                                                            TISSUE—Ovarian carcinoms;

RA ISSUE—Ovarian carcinoms;

RA Nishikawa T., Nagaik K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nishikawa T., Nagaik K., Sugano S., Shiratoria A., Sudo H.,

RA Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Ra Aranabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

RA Maranabe S., Kimura K., Marakami K., Ishii S., Kawai Y., Saito K.,

RA Mamonto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA NHO-DEPENDENT BANNER TO RECHUT PROFILIN TO THE MEBRANE, WHERE

SUBmitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

I. FUNCTION: BINDS TO GTP-BOUND FORM OF RHO AND TO PROFILIN. ACTS IN

A RHO-DEPENDENT MANNER TO RECRUIT PROFILIN TO THE MEBRANE, WHERE

IT PROMOTES ACTIN POLYMERIZATION IT IS REQUIRED FOR CYTOKINESIS,

STRUM RESPONSE FACTOR. DER PROTEINS COUPLE RHO AND SRC TYROSINE

STRUM RESPONSE FACTOR. DER PROTEINS COUPLE RHO AND SRC TYROSINE

STRIABEL DURING SIGNALING AND TRANSCRIPTION OF ACTIN DYNAMICS (BY

STRILARITY). IN HEARING TH MAY PLAY A ROLE IN THE REGULATION OF

ACTIN POLYMERIZATION IN HAIR CELLS.

KINDES SPECIFETITY: EXPRESSED IN BRAIN, HEART, PLACENTA, LUNG,

KINDEY, PANCREAS, LIVER, SKELETAL, MUSCLE, AND COCHLEA.

CHOMAIN: DRES ARE REGULATED BY INTRAMOLECULAR GBD-DAD BINDING WHERE

RHO-GET ACTIN DELINATES THE DRES BY DISRUPTING THE GBD-DAD BINDING WHERE

RHO-GET ACTIN DELINATES THE DRES BY DISRUPTING THE GBD-DAD BINDING WHERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                               SEQUENCE FROM N.A.
MEDLINE-98028756; PubMed-9360932;
Lynch E.D., Lee M.K., Morrow J.E., Welcsh P.L., Leon P.E., King M.-C.;
"Nonsyndromic deafness DFNAl associated with mutation of a human homolog of the Drosophila gene diaphanous.";
Science 278:1315-1318(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN THAT IT SEEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN DIAPHI ARE A CAUSE AUTOSOMAL DOMINANT MONSYNDROMIC SENSORINEURAL DEAFNESS I (DFWAI).
SIMILARITY: CONTAINS I GTPASE-BINDING DOMAIN (GBD).
SIMILARITY: CONTAINS I FORMIN HOMOLOGY I (FHI) DOMAIN.
SIMILARITY: CONTAINS I FORMIN HOMOLOGY 3 (FH2) DOMAIN.
SIMILARITY: CONTAINS I DREWIN HOMOLOGY 3 (FH2) DOMAIN.
SIMILARITY: CONTAINS I DRE AUTOREGULATORY DOMAIN (DAD).
SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. DIAPHANOUS
                 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSKA (IN REF. 2).
ED1F5147CFF9A886 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARG/LYS-RICH (BASIC).
T -> TSKA /IN PER ?:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PRO-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK023345; BAB14533.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO INCLUDE INTRONIC SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138978 MW;
                 Chordata;
Primates;
                                                                                                                                                                                                  SEQUENCE OF 218-817 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deafness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF051782; AAC05373.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003104; -. Pfam; PF02181; FH2; 1.
   sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                 Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK023345;
MIM; 602121; -.
MIM; 124900; -.
                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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34;
                                                                                                                                        : | : | : | | | | 308 LINALITPAEELDFRVHIRSELMRLGLHQVLQDLREIENEDMRVQLNVFDEQGEEDSYDL 367
                                                                                                                                                                                                             ---LQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYDVCEQPPPLNILTP---YRDDGK 145
                                                                                                                                                                                                                                                              368 KGRLDDIRMEMDDFNEVFQ-----ILLNTVKDSKAEPHFLSILQHLLLVRNDYE 416
                                                                                                                                                                                                                                                                                                                     146 EGLKFY-------TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLD 185
                                                                                                                                                                                                                                                                                                                                                                      417 ARPQYYKLIEECISQIVLHKNGADPDFKCRHLQIEIEGLIDQMIDKTKVEKSEAKAAELE 476
                                                                                                                                                                                                                                                                                                                                                                                                                          186 RPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQTYVDH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 MDGSYSLSALPFSQMSELLTRAEE-----RVLVRPHEP----PPPPPMHGAGD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPPPSALSTSSLRASMTSTPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPP----PPLPPPGIRPSSPVTVT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PP----VPPPPPP-PPATALQAP-----AVPPPPAPLQIAPGVLHPAPPPIAPPL-- 393
                                                                                                        -----DRLSVSVTQLDPKEEELS--- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKLDSELTAR--HELQVEMKKMESDFEQKLQDLQ-----GEKDALHSE-KQQIATEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 ALAHPPSGLHPTPSTAPGPHVPLMPP----SPPSQVIP-ASEPKRHPSTLPVISDARSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein gene in lateral root initiation.";
Genes Dev. 3:1639-1646(1989).
-!- FUNCTION: HAS A SECTIALIZED STRUCTURAL FUNCTION, POSSIBLY IN
THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
                                                    Indels 199;
Length 1248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV, XANTHI; TISSUE-Leaf;
MEDLINE-90128253; PubMed-2612909;
KEller B., Lamb C.J.;
"Specific expression of a novel cell wall hydroxyproline-rich
                                                      Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502 LEAIRKGIQLRK-----VEEQREQE----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LYKPEVOLRRPNWSKLVAEDLSQDCFWTKVKEDRFENN 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAIN ROOT.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
Score 313.5; DB
Pred. No. 3.7e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicotiana tabacum (Common tobacco)
                                                                                                        IFGELFNEAHSFSFRVNSLQERV---
                                                    58;
10.5%;
25.2%;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4097;
                                                      146;
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  Query Match
Best Local S
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                                                      Matches
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Query Match
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                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement from the commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        15;
PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
                                                                                                                                                                                                                      H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 SPPPPAYSPPPSPIYSPPPPQVQPLPPTFSPPPPRRIHLPPPPHRQPRPTTYGQPPS 532
                                                                                                                                                                                                                                                                                                                                                                                             279 PPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPT------PPPP-- 327
                                                                                                                                                                                                                                                                                                                                                                                                             328 --PPPLPSALSTSSLRASMTSTPPPPV---PPPPATALQAP---AVPPPPAPLQ 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAPGVLHPAPPPI----APPLVQPSPPVARAAP---VCETVPVH--PLPQGEVQGLPPP 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P----PPPPL-----PPPGIRPSSPVTV-----TALAHPPSGLH--PTPSTAPGPHV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 PPTFSPPPPRQIHSPPPHWQPRTPTPTYGQPPSPPTFSAPPPRQIHSPPPHRQPRPPT 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last annotation update)
MISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).
WAS OR WASP.
WAS OR WASP.
WAS OR WASP.
BUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
MCBL_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C;
MEDLINE-96115600; PubMed-8666397;
Derry J.M.J., Wiedemann P., Blair P., Wang Y:, Kerns J.A.,
Lemahieu V., Godfrey V.L., Wilkinson J.E., Francke U.;
"The mouse homolog of the Wiskott-Aldrich syndrome protein (WASP)
                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                               CONTAINS THE SER-PRO(4) REPEATS.

3 X APPROXIMATE TANDEM REPEATS.

641DD2278AB28524 CRC64;
                                                                                                                                                         PIR; S06733; S06733.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
Hydroxylation.
                                                                                                                                                                                                                                                                                                                                         10.4%; Score 309; DB 1; Length 620; llarity 34.7%; Pred. No. 3e-08; Conservative 9; Mismatches 90: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 AA.
                                                                                                                                                                                                            EXTENSIN.
                                                                                                                                                                                                                                                                                                          ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593 PIYGQPPSPPTTYSPPSPP 611
                                                                                                                                             EMBL; X13885; CAA32090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 PL--MPPSPPSQVIPASEP 484
                                                                                                                                                                                                                                                                                                         65406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
                                                                                                                                                                                                                                            229
229
236
205
499
620 AA;
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WASP_MOUSE
P70315;
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Si
Matches 90;
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WASP_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 QRQSGERRQLPPPPAPINEERRGGLPPVPPHPGGDHGGPSGGPLSLGLVTVDIQNPDITS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMH------GAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPP---- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 PCRGGGGGGGGGGGGGGGGQPL------RP--PVVGSNKGRSGPLPPVPMG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 GAPPPTPRG------PPPPGRGGPPPPPPATGRSGP--PPPPLPGAGGP-- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QETYDVCEQPPPLNILTPY-----RDDGKEGLKF--YTNPSYFFDLWKEKMLQDTEDKRK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 QELYSQLVYLTP----TPFFHTFAGDDCQVGLNFADESEAQAFRALVQEKI-----QKRN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 -PPPPPLPSALSTSSLRASMTSTPPPP---VPPPPPPPATALQAPAVPPPPAPLQIAPGV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 LHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSS 441
                                                                       -!- FUNCTION: POSSIBLE REGULATOR OF LYMPHOCYTE AND PLATELET FUNCTION MAY BE INVOLVED IN SIGNALING PATHWAYS WITH CYTOSKELETAL FUNCTION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 SRYRGLPAPGPGPTDKKRSGKKKISKADIGAPSG---FKHV-----SHVGWDPQNGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------APHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQTYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 HMDGSYSLSALPFSQ--MSEL-LTRAEERVLV--------RPHE--PPPPP
                                                                                                                                                 -!- DOMAIN: THE WHI (WASP HOMOLOGY 1) DOMAIN MAY BIND A PRO-RICH
gene is highly conserved and maps near the scurfy (sf) mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138; Indels 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASP/GLU-RICH (ACIDIC).
9C223733C59F0C8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.0%; Score 297; DB 1; 24.3%; Pred. No. 9.4e-08; iive 36; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GBD.
GRSGPLPPXP M
GRSGPLPPXP M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY - PRO.
                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 GBD DOMAIN.
-!- SIMILARITY: CONTAINS 1 WH1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 EKRKQKQKNLDRPHEPEKVPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U54788; AAC52556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390
403
424
520
54191
                      the X chromosome.";
Genomics 29:471-477(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50108; GBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408
503
520 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354
393
                                                                                                                                                                                  LIGAND
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PPPPSTIPLIPPFTG-GFLPPLPGSKLPDFAGLLPLIPNLPDVPPIGGGPPVNQPKPSSP 142

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                                                                   452
                                                        442 PVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVL 501
                                                                                                                                                                                                                                       453 LDQIRQGIQLNKTPGALENSVQQPPAQQSEGLVGALMHVMQKRSRVIHSSDEGEDQTGED 512
-----ppppppp------ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTENSIN-LIKE PROTEIN.
                                                                                                                ------PCPGSGPAP----PPLPPTPVSGGS-----PAPGGGRGAL
                                                                                                                                                                           LEAIRKGIQLRKVE---EQREQEAKHERIENDVAT---ILSRRIAVEYSDSE-----DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
51A495CC94017812 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 286.5; DB 1; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PISTIL-SPECIFIC EXTENSIN-LI
4 X 5 AA REPEATS OF S-P(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000419; -.
Pfam; PF01190; Pollen_Ole_e_I; 1.
Structural protein; Signal; Repeat; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. PETITE HAVANA; TISSUE-PISTII; MEDLINE-93005740; PubMed-1392607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -JUN-1994 (Rel. 29, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z14019; CAA78397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Begt Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  556
                                                                                                                                                                                                                                                                                                                                                           513 EEDDEWD 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                  SEFDEVD
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EXLP_TOBAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- ALTERNATIVE PRODUCTS: AT LEAST 5 ISOFORMS; IA (AC Q05860), IB (AC Q05860), II (AC Q05860), AND IV (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. A VARIATION IN SPLICING IS SEN AMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE.
-!- TISSUE SPECIFICITY: IT IS FOUND THROUGHOUT THE EMBRYO BUT HAS A FUNCTIONAL ROLE ONLY IN THE ISOFORM FOUND. IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL COMPARTMENT OF THE DEVELOPING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grusby-Jackson L., Kuo A., Leder P.;
"A variant limb deformity transcript expressed in the embryonic mouse limb defines a novel formin.";
Genes Dev. 6:29-37(1992).
  ----PPPPPPLPSALSTSSLRASMTSTPPP---PVPPPPPPPATA-LQAPAVPPPPAPL 375
                                                                                                                                                        PGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVI 494
                                                                                                                                                                                             243 VMTPSPSPA----AEPPI-IAPFPSPPANP--PLIPRRPAPPVVKPLPPLGKP---PIV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: IS IMPORTANT IN THE MORPHOGENESIS OF LIMB AND MAY HAN FUNCTION IN DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- PTM: PHOSPHORYLATED ON SERINE AND POSSIBLY THREONINE RESIDUES.
-:- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
-:- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-:- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO SUBFAMILY.
                    143 SPLVKPPPPPSPCKPSPPDQSAKQPPPPAKQPSPPPPPP-
                                                                           QIAPGVLHPAPPPIA-PPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPP
                                                                                                                 ---PPVKAPSPSPATQPPTKQPPPP------PRAKKSPLLPPPPVAYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORMIN I ISOFORM IV (LIMB DEFORMITY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Embryo;
MEDLINE=92112033; PubMed=1339380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X62379; CAA44244.1; -.
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:101815; Fmn.
InterPro; IPR001265; -.
InterPro; IPR003104; -.
Pfam; PF02181; FH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                       FM14_MOUSE
ID FM14_MOUSE
AC Q05859;
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13;

Gaps

55;

Indels

91;

Pred. No. 2.4e-07, Mismatches 9

11;

ilarity 34.9%; Conservative

----PPMHGAGDAKPIPTC----ISSATGLIENRPQSPATGRTPVFVSPTP

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19;
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043516; 09GNP1; 015220;
01-007-2000 (Rel. 40, created)
01-007-2000 (Rel. 40, Last sequence update)
01-007-2000 (Rel. 40, Last annotation update)
WISKOTT-ALDRICH SYNDROME PROTEIN INTERACTING PROTEIN (WASP INTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582
                                                                                                                                                                                                                                               SVTQLDPKEEELSLQDITMR--KAFRS---STIQDQ-QLFDRKTLPIPLQETYDVCEQPP 132
                                                                                                                                                                                                                                                                 348 -LNIDMPRTEQKEADPEFHGADEMGYSTDQESHKSPRDAHVQGGQVKARTPETALEAFKA 406
                                                                                                                                                                                                                                                                                                                                                                                            407 LFIRPPKKGSTADISELEALKRKMKHEKESLRAVFERSKSRPADSPSDPKSPDQSPTEQD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 ATGRTPVFVSPTPPPPPPPPPALSTSSLRASMTSTPPPPPP------PPPPPATAL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'MEDLINE-98070810; PubMed=9405671;
Ramesh N., Anton I.M., Hartwig J.H., Geha R.S.;
"WIP, a protein associated with Wiskott-Aldrich syndrome protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPPPPPPPLPPPGIRPSSPVTVTALAHPPSGLH--PTPSTAPGPHVPLMPPSPP 475
                                                                                                                                                                                                                     195;
                                                                                                                                                                                        Length 1206;
             Developmental protein; Alternative splicing;
                                                                                                                                                                                                                     Indels
                                                                                                                                               4DFB38CB52BD8EE7 CRC64;
                                         COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                         COILED COIL (POTENTIAL).
                                                                                                                                                                                                                   167;
                                                                                                                                                                                         DB 1;
                                                                                                                                                                                      9.6%; Score 286.5; DB :
llarity 21.9%; Pred. No. 6.6e-07,
Conservative 55; Mismatches 16
                                                                      FH1 (PRO-RICH)
FH2.
                                                                                                                                 POLY - SER
                                                                                                                                                                                                                                                                                                        133 PLNILTPYRDDGKEGLKFY------
                              Coiled coil
                                                                                                                                             133464
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FORMIN
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11164
11116
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                                                                                                                                               AA;
                                                                                                                                                                                                     Similarity
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PR00828;
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                                                                                                               635
                            Phosphorylation
                                                                                                                                                                                     Query Match
Best Local Simi
Matches 117;
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            Nuclear
PRINTS;
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J. Immunol. 162:5019-5024(1999).
J. Immunol. 162:5019-5024(1999).
J. PUNCTION: MAY HAVE DIRECT ACTIVITY ON THE ACTIN CYTOSKELETON.
INDUCES ACTIN POLYMERIZATION AND REDISTRIBUTION. THYMUS. LOWER EXPRESSION IN OVARY, HEART, BRAIN, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, TESTIS. Stewart D.M., Tian L., Nelson D.L.; "Mutations that cause the Wiskott-Aldrich syndrome impair the interaction of Wiskott-Aldrich syndrome protein (WASP) with WASP 90; G -> A.
/FTIG=VAR_010295.
PRRPHLR -> SSQAPPP (IN REF. 3).
P -> PV (IN REF. 2).
GSNRRRGGPPLPPIPR -> EYFCQGF (IN 43EB88674DD3BFIA CRC64; -!- SUBDNIT: BINDS TO WASP, PROFILIN AND ACTIN. -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PERIPHERAL BLOOD MONONUCLEAR CELLS, SPLEEN, PLACENTA, SMALL INTESTIN, COLG ; Score 284; DB 1; Length 503; ; Pred. No. 3.7e-07; 25; Mismatches 124; Indels 9 Kreideweiss S., Delany-Heiken P., Nordheim A., Ruhlmann A.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. AND VARIANT ALA-495. Induces actin polymerization and redistribution in Proc. Natl. Acad. Sci. U.S.A. 94:14671-14676(1997) XRSGPXPPXP MOTIF 1. XRSGPXPPXP MOTIF 2. XRSGPXPPXP MOTIF 3. ACTIN BINDING. GLY-RICH. POLY-SER. PRO-RICH MEDLINE-99218549; PubMed-10202051; [3] SEQUENCE OF 192-503 FROM N.A., EMBL; AF031588; AAC03767.1; -. FMRL; AF106062; AAD45972.1; -. ΨW, 9.5%; 360 503 51489 1 X86019; CAA60014.1; Query Match 9.59 Best Local Similarity 29.99 Matches 102; Conservative InterPro; IPR003124; - Pfam; PF02205; WH2; 1. Actin-binding; Repeat. 413 419 48 495 361 309 360 487 503 AA; [2] SEQUENCE FROM N.A. 64 241 264 352 374 410 45 495 MIM; 602357; CONFLICT CONFLICT SEQUENCE CONFLICT REPEAT REPEAT SITE: VARIANT DOMAIN DOMAIN DOMAIN DOMAIN REPEAT EMBL; 348 g QQ g pp ò ò ò

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WAS OR IMD2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT
2) (SF3A66).
428 -PPPPL-PPPG----IRPSSPVT----VTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQV 478
            --IDYPEIAEGIMPRHRFMSAYEQRIEPPDRR~-WQYLLMAAEPYETIAFKVPSREIDKA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 QETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKQKQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 KEAKEAPAQPAPEKVKVEVKKFVKIG-----RPGY----KVTKQRDTEMGQQSLLFQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%; Score 281; DB 1; Length 485; Best Local Similarity 28.3%; Pred. No. 4.9e-07; Matches 125; Conservative 31; Mismatches 152; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     processing; mRNA splicing; Nuclear protein; Repeat.
IN 233 236 POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70D2CAE4FC938458 CRC64;
                                     479 IPASEPKRHPSTLPVISDARSVLLEAIRKGIQLRKVEEQRE 519
                                                    SAGAPPPPPST-----SIRNGFODSPCEDEWE 451
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POLY-PRO.
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                           Created)
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                                                                                                        STANDARD;
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(Rel. 35,
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485 AA;
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SF3A2 OR SAP62.
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Q62203;
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MEDLINE-95273432; PubMed-7753869; Kwan S.P., Hagemann T.L., Radtke B.E., Blaese R.M., Rosen F.S.; "Identification of mutations in the Wiskott-Aldrich syndrome gene and characterization of a polymorphic dinucleotide repeat at DXS6940, adjacent to the disease gene.";
       ----KPPAPPSLPAGPPGV 230
                                                                           --PPPPPPMHGAGDAKPIPTCISSAT--GLIENRPQSPATGRTPVFVSPTPPPPPPPPLPSA 334
                                                                                                                                                                                                           LSTSSLRASMTSTPPPPVP---PPPATALQAPAV---PPPPAPLQIAPGVLHPA 385
                                                                                                                                                                                                                                                      P---PPIAPPLVQPSPPVARAAP------VCETVP-VHPLPQGEVQ----GLPPP--- 426
                                                                                                                                                                                                                                                                                                                                                                                           -----PPPPP-----PLPPPGIRPSSPVTVTALAHP-PSGLHPT-PSTAPGP 465
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                                                                                                                                       231 KRPPPPLMNGLPPRPPLPDALPPPPGGL--PLPPMPPTGPAP-SGPPGPPQMPPPAPGV 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ű.
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VARIANTS WAS F-27; I-48; M-75; L-86; H-86; K-131; C-187 AND K-477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Derry J.M.J., Ochs H.D., Francke U.; "Isolation of a novel gene mutated in Wiskott-Aldrich syndrome."; Cell 78:635-644(1994).
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adjacent to the disease gene.";
Proc. Natl. Acad. Sci. U.S.A. 92:4706-4710(1995)
EG-----KFWTHWNRETKOFFLOFHFKME-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derry J.M.J., Ochs H.D., Francke U.; Cell 79:923-923(1994).
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Hum. Mol. Genet. 4:1119-1126(1995).
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MEDLINE-94349367; PubMed=8069912;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 MPPMLRPPLPSDGPGNMPPPPP 483
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MEDLINE-98378988; PubMed-9713366; Facchetti.F., Blanzuoli L., Vermi W., Notarangelo L.D., Giliani S., Fiorhini M., Fasth A., Stewart D.M., Nelson D.L.; "Defective actin polymerization in EBV-transformed B-cell lines from J. Pathol. 185:99-107(1998).
                                                                                                                                                                               Ugazio A., Vezzoni P.;
X-Iinked thrombooytopenia and Wiskott-Aldrich syndrome are allelic
diseases with mutations in the WASP gene.";
Nat. Genet. 9:414-417(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS WAS MET-75; LEU-84; ASP-89 AND LYS-133.
MEDLINE-98350091; PubMed-9683546;
MacCarthy-Morrogh L., Gaspar H.B., Wang Y.-C., Katz F., Thompson L.
                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS WAS LYS-31 AND MET-45.
MEDLINE-97253413; PubMed-9098856;
Ariga T., Yamada M., Sakiyama Y.;
"Mutation analysis of five Japanese families with Wiskott-Aldrich syndrome and determination of the family members' carrier status using three different methods.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Layton M., Jones A.M., Kinnon C.;
"Absence of expression of the Wiskott-Aldrich syndrome protein in peripheral blood cells of Wiskott-Aldrich syndrome patients.";
Clin. Immunool. Immunootthol. 88:22-27(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99374925; PubMed-10447259; Lemahleu V., Gastler J.M., Francke U.; Novel mutations in the Wiskott-Aldrich syndrome protein gene and their effects on transcriptional, translational, and clinical
                                                                                                                                                                                                                                                                            MEDLINE-97272113; PubMed-9126958; Remold-0'Donnall E., Cooley J., Shcherbina A., Hagemann T.L., Keman S.-P., Kenney D.M., Rosen F.S., "Variable expression of WASP in B cell lines of Wiskott-Aldrich
           Derry J.M.J., Kerns J.A., Weinberg K.I., Ochs H.D., Volpini V., Estivill X., Walker A.P., Francke U.; "WASP gene mutations in Wiskott-Aldrich syndrome and X-linked
                                                                                                                                             Villa A., Notarangelo L., Macchi P., Mantuano E., Cavagni G.,
Brugnoni D., Strina D., Patrosso M.C., Ramenghi U., Sacco M.G.,
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Parolini O., Ressmann G., Haas O.A., Pawlowsky J., Rnapp W., Holter W. T., T. Linked Wiskott-Aldrich syndrome in a girl.";
New Engl. J. Med. 338:291-295(1998).
                                                                                                                                                                                                                                                               VARIANTS WAS TRP-43; MET-45; MET-75 AND CYS-86.
                                                                              Mol. Genet. 4:1127-1135(1995)
                                                                                                                               MEDLINE=95315993; PubMed=7795648;
MEDLINE=96133286; PubMed=8528199;
                                                                                                                                                                                                                                                                                                                                                            Immunol. 158:4021-4025(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pediatr. Res. 41:535-540(1997)
                                                                                                              VARIANTS WAS V-56 AND E-236
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                                                              thrombocytopenia.
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DIARRHEA. DEATH USUALLY OCCURS BEFORE AGE 10.
DISEASE: DEFECTS IN WASP ARE THE CAUSE OF ISOLATED X-LINKED THROMBOCYTOPENTA (XIT). XLT IS CLINICALLY MILD WITH SMALL PLATELETS AND SUBCLINICAL LEUKOCYTE ABNORMALITIES.
SIMILARITY: CONTAINS 1 GBD DOMAIN.
SIMILARITY: CONTAINS 1 WHI DOMAIN.
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E -> K (IN WAS).
FTId=VAR_005825.
C -> W (IN WAS; MODERATE FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN THROMBOCYTOPENIA)
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/FTId=VAR_005827.
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V -> M (IN THROMBOCYTOPENIA).
/FTId-VAR_005828.
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F -> L (IN WAS; SEVERE FORM).
/FTId=VAR_008109.
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/FTId=VAR_005829.
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3 -> D (IN WAS; MILD FORM).
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W -> C (IN ATTENUATED WAS).
/FTId=VAR_005833.
E -> K (IN WAS).
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GRSGPLPPXP M
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InterPro; IPR001960; -.
Pfam; PF00786; PBD; 1.
Pfam; PF000568; WH1; 1.
PROSITE; PS50108; GBD; 1.
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228; Gaps 25; DTEDKRK 174 1 1	ATVDIQNPDITS 209 SHFETRPQTYVD 244	IAPPLVQ 395 387 AHPPSGL 455PSSGN 408 IQLRKVE 515		P.J., .n C., is genome.";
/FTId=VAR_005834. E -> K (IN WAS; SEVERE FORM). /FTId=VAR_005835. G -> C (IN WAS). /FTId=VAR_005836. A -> E (IN THROMBOCYTOPENIA). /FTId=VAR_05837. ; Score 280; DB 1; Length 502; Pred. No. 5.7e-07; / Pred. No. 5.7e-07; // Mismatches 142; Indels 37; Mismatches 142; Indels FDGKEGIKFYTNPSYFFDLWKEKMLC	15		T 12 EBN2_EBV STANDARD; PRT; 487 AA. EBN2_EBV STANDARD; PRT; 487 AA. p12978; 01-OCT-1989 (Rel. 12, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 01-OV-1995 (Rel. 32, Last annotation update) 01-NOV-1995 (Rel. 32, Last annotation update) EBNA-2 NUCLEAR PROFEIN. BYRRI. Epstein-barr virus (strain B95-8) (Human herpesvirus 4). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.	SEQUENCE FROM N.A. MEDLINE-84270667; PubMed-6087149; MEDLINE-84270667; PubMed-6087149; MEDLINE-84270667; PubMed-6087149; Bager R., Bartell P.J., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."; Nature 310:207-211(1984). [2] SUBCELLUIAR LOCATION, AND PHOSPHORYLATION. MEDLINE-90266473; PubMed-2161150;
VARIANT 133 133 VARIANT 187 187 VARIANT 236 236 Query Match Best Local Similarity 23 68 Matches 126; Conservative 122 QETYDVCEOPPENILTPY 199 QELYSQLVYSTPTPFFPH	175 EKRKOKOKNLDRPHEPEKVPR :::	339 SLRASMISTPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	RESULT 12 EBN2_EBV TD EBL2_EBV STANDARD DT 01-0CT-1989 (Rel. 12, C DT 01-0CT-1989 (Rel. 12, L DT 01-NOV-1985 (Rel. 32, L DE EBNA-2 NUCLEAR PROTEIN. GN BYRF! OC VILUSES; GSDNA VILUSES; OC VILUSES; GSDNA VILUSES; OC Gammaherpesvirinae; Lym OX NCBI_TAXID=10377;	MEDLINE-84270667; PubMed-6087149; Bacr R., Bankler Arr., Biggin M.D., Gibson T.J., Hatfull G., Hudson G.S. Tuffnell P.S., Barrell B.G.; "Nature 310:207-211(1984). [2] SUBCELLULAR LOCATION, AND PHOSPHORYIMEDLINE-90266473; PubMed-2161150;
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J.I., Wang F., Kieff E.;
in-Barr virus nuclear protein 2 mutations define essential
is for transformation and transactivation.";
ol. 65:2345-2554(1991).
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1. Similarity 27.1%; Pred. No. 9e-07;
98; Conservative 24; Mismatches 73; Indels 167; Gaps
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infection nuclear proteins.";
yg 176:563-574(1990).
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               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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-i- SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-i- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO SUBFAMILY.
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EMBL; AE003578; AAF51054.1;

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94 DITMRKAFRSS--TIQDQ-----QLFDRKTLPIPLQETYDVCEQPPPLNILTPYRDDGK 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 -----TTP-----LLSSNVLKKVASFTVEKSSAGNNSSNPPNLCPTSDETTLLATPCSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 SLTVATLPPEIAVGAAAGGVAGGAGSRRGSSXVPEKLSFAAYEKFEGQMLIKWLISTMQS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 NPKSSSGDANQELFNTLALQFCNNLKYVGVLKQISNEHLDCGFSPYEMYQWTHTEQPTTS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QOILKKRLLINCTTLAEVHAVVNELLSSVDEPPRRPSKRCVNLTELLNASEATVYEYNKTG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETPLDNIDEFTELFSRQAIAPVSKPKELKVKRAKSIKVLDPERSRNVGIIWRSLHVPSSE 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2e-06;
ches 219; Indels 344; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            ---STO- 93
                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EW-----EW--OKLAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 WIRIVISAPPAPRPPSVANSTDSTENSGSSPDEPPAANGADAP--PTAPPATKEIWTEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GPELAEDDAN-----TRPQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 PPL----VQPSPPVARAAPVCETVPVHPLP---QG------EVQGLPPPPPPPL-
                                                                                                                                                                                                                                                                                                                             DB 1; Length 1059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------QVIPASEPK----RHPSTLPVISDARS-----
                                                                                                                                      S -> C (IN REF. 1).
S -> T (IN REF. 1).
T -> S (IN REF. 1).
E -> K (IN REF. 1).
H -> P (IN REF. 1).
MISSING (IN REF. 1).
WM : 009B0E24F6IB6EAS CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                            53 GELFNEAHSFSFRVNSLQER----VDRLSVSVTQLDPKEEEL-
                                                                                                                                                                                                                                                                                                                                               20.1%; Pred. No. 2e-00
tive 73; Mismatches
                                                                                                    FH1 (PRO-RICH)
FH2.
                                                                                                                                                                                                                                                                                                                             Score 275;
                                                                                                                                                                                                                                                                                                                                9.28;
                                                                                                                                                                                                                                                                  113863
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
IPR001265; -.
                                                           PRINTS; PR00828; FORMIN
                                        Pfam; PF02181; FH2; 1.
                                                                                 Developmental protein
                                                                                                                                                                                                                                                                1059 AA;
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                            98
                                                                                                                                                                                     988
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Best Local Simi
Matches 160;
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FMN1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                             the cellular compartment.";
J. Cell Biol. 109:349-3501(1989).
-!-FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C32 STRUCTURE). THE
COVALENT CORSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
RATHER THAN BETWEEN THE POLYDEPTIDE CHAINS.
-!- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
HYDROXYPROLINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 PNNSPLPP-----SPOPTASS-----RPPSPPP----SPRPPSPPSPS- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 PHEPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPSA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 LSTSSLRASMTSTPPPPPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPLV 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RKPPS- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Indels 115; Gaps
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=F. NAGARIENSIS / HKIO.
MEDLINE=90094551; PubMed=2689458;
Ertl H., Mengele R., Wenzl S., Engel J., Sumper M.;
"The extracellular matrix of Volvox carteri: molecular structure of the cellular compartment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 QPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSSPVTVTALAHPPSG
                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.2%; Score 273.5; DB 1; Length 485; Best Local Similarity 33.8%; Pred. No. 1.1e-06; Matches 76; Conservative 5; Mismatches 29; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A52216400A031421 CRC64;
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                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SULFATED SUFFACE GLYCOPROTEIN 185 (SSG 185).
VOLVOX carteri.
                                                                                                                                   485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Sulfatation; Hydroxylation. DOMAIN 228 340 PRO-RICH.
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                                                                                                                                     PRT;
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536 SRRIA-----VEYSDS 546
                                  778 SERISCIVFQAEFEES 793
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A33647; A33647
                                                                                                                                   SSGP_VOLCA
P21997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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FMN1_MOUSE
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                                                                                                           SSGP_VOLCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

1. Proc. Natl. Acad. Sci. U.S.A. 90:5554-5558(1993).

2. I. FUNCTION: IS IMPORTANT FOR THE MORPHOGENESIS OF LIMB AND KIDNEY AND MAY HAVE BY FUNCTION IN DIFFERENTIATED CELLS OR MAY BE INVOLVED IN MAINTAINING SPECIFIC DIFFERENTIATED STATES.

2. SUBCELLULAR LOCATION: NUCLEAR.

3. SUBCELLULAR LOCATION: NUCLEAR.

4. VARIATION HARDOUTS: AT LEAST 5 ISOFORMS; IA (SHOWN HERE), IB, II, III AND IV (AC Q05659); ARE PRODUCED BY ALTERNATIVE SPLICING. A VARIATION IN SPLICING SEEN AMONG DIFFERENT TISSUES AND DIFFERENT SIZES TRANSCRIETS EXIST WITHIN ANY ONE TISSUE.

2. I. TISSUE SPECIFICITY: IT IS PRESENT IN THE ADULT KIDNEY, TESTIS, LIMB, OVARY, BRAIN: SMALL INFESTINE, SALIVARY GLAND AND HARDERIAN GLAND.

3. IL SEXPRESSED IN THE APICAL ECTODENAAL RIDGE AND THE MESENHYMAL COMPARTMENT. IN THE POSTERIOR ECTON. DURING KIDNEY MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS.

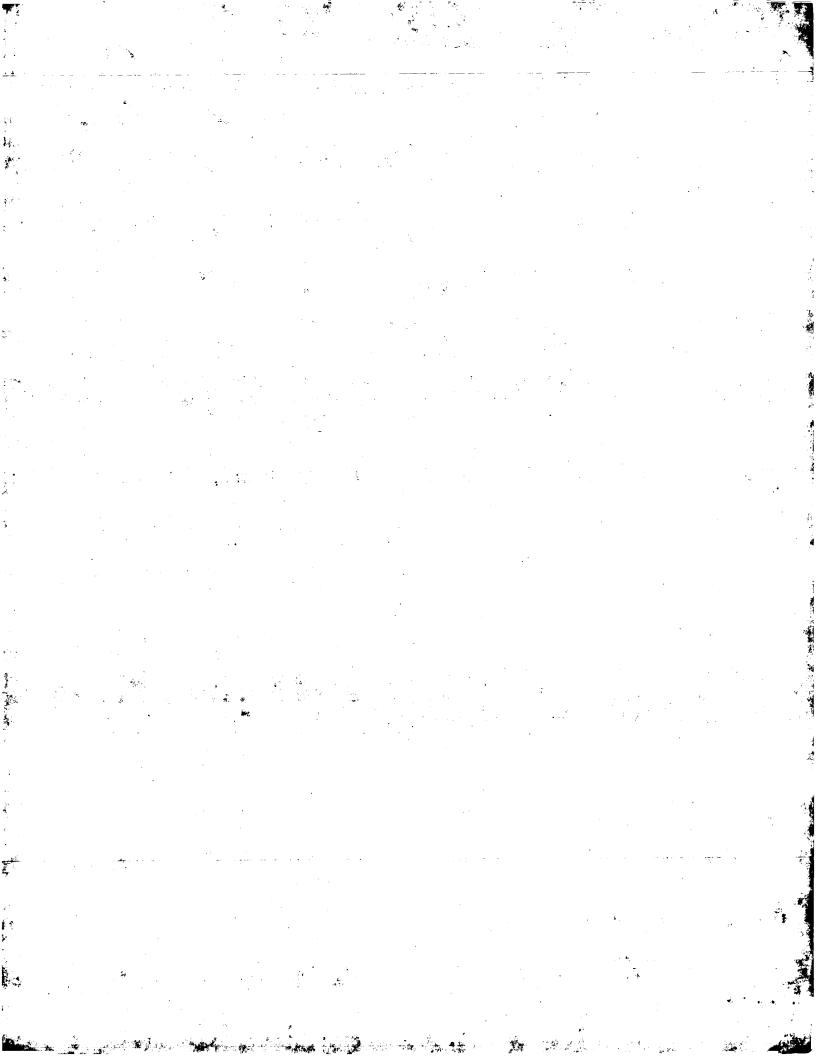
3. THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.

4. SIMILARITY: CONTAINS I FORMIN HOMOLOGY 2 (FH1) DOMAIN.

5. SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY 2 FAMILY. CAPPUCCINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vogt T.F., Jackson-Grusby L., Rush J., Leder P.;
"Formins: phosphoprotein isoforms encoded by the mouse limb deformity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Woychik R.P., Maas R.L., Zeller R., Vogt T.F., Leder P.; "Permins: proteins deduced from the alternative transcripts of the limb deformity gene,"; Nature 346:850-853(1990).
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALTERNATIVE SPLICING.
MEDLINE=97224459; PubMed=9119367;
Wang C.C., Chan D.C., Leder P.;
"The mouse formin (Fmn) gene: genomic structure, novel exons, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0828; FORMIN.
Nuclear protein; Developmental protein; Alternative splicing;
Phosphorylation; Coiled coil.
DOMAIN 723 792 COILED COIL (POTENTIAL).
                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-3000 (Rel. 40, Last annotation update)
FORMIN 1 ISOFORMS I/II/III (LIMB DEFORMITY PROTEIN).
PRT; 1468 AA.
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PHOSPHORYLATION,
MEDLINE-93296176; PubMed-8516300;
MEDLINE-93296176; PubMed-8516300;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Kidney, and Testis;
MEDLINE-90363291; Pubmed-2392150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X53599; CAA37668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic mapping.";
Genomics 39:303-311(1997).
STANDARD;
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MGD; MGI:101815; Fmn.
InterPro; IPR001265; -.
InterPro; IPR003104; -.
                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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HIDDRY REPRESENTED BY THE PROPERTY OF THE PROP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 APLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPL 432
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|-----NSGGPPPPPPPP 959
                                                                                                                                                                                                                                                                                                          9.1%; Score 272.5; DB 1; Length 1468;
23.0%; Pred. No. 3.6e-06;
tive 50; Mismatches 173; Indels 181; Gaps
                                                                                                                                                                                                                                                                                                                                                                             53 GE-LFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQL 111
                                                                                                                                                                                                                                                                                                                                                                                                             549 GEVVFNEYPSRKNDVSSGFPSADTL------EPSSTTKVTETKGASPTSLRASQ- 596
                                                                                                                                                                                                                                                                                                                                                                                                                                              112 FDRKTLPIPLQETYDVCEQPP----PLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKML 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TWLVSEEASEKGLGPEKITAPPQHQLPPGI---ASEGFPCDNFKEQTA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 QDTEDK-----RKEKRKQKQKNLDRPHEPEKVPRAPHDR-----RR 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702 VWPPPKTKDTEEKVGLKYTEAEYQAAILHLKREHKEEIETLQAQFELK--TF--HIRGEH 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLSALPFSQMSELLTRAEER-----VLVRPHEPPPPPPMHG---------286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 ALVTARLEEAIENLKQQLEKRREGCEEMRDVCISTDDDCSPKAFRNVCIQTDRETFLKPC 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGDAKPIPTCISSATGLIENRPQSPATGRTPVFV 320
FH1 (PRO-RICH).
FH2.
COILED COIL (POTENTIAL).
POLY-SER.
POLY-PRO.
POLY-SER.
MISSING (IN ISOFORM II).
IA -> SV (IN ISOFORM III).
MISSING (IN ISOFORM III).
MISSING (IN ISOFORM III).
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v; 163809 1
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Search completed: June 20, 2001, 12:10:54 Job time: 194 sec



34 9 1.6 412 1 ALF 35 9 1.6 421 1 ACR 36 9 1.6 435 1 KIG 37 9 1.6 440 1 EXG 39 9 1.6 440 1 G3F 40 9 1.6 450 1 CYS 41 9 1.6 487 1 EBN 42 9 1.6 520 1 WAS 44 9 1.6 515 1 PPR 45 9 1.6 518 1 TPR	30L	KIAA0269 KIAA0269 EUKATYOTA; M MAMMAIIA; EU NOBI_TAXID-9 (1) SEQUENCE FRO SEQUENCE FRO SEQUENCE TRO SEQUENCE TO SEQUENCE TO NAQASE T. TO NAQASE	CC This STMILEATIVE TO C. ELEGENS ROCC This STMILEATIVE TO C. ELEGENS ROCC This STMICATIVE TO C. ELEGENS ROCC This SWISS PROT entry is copyrided to between the Swiss Institute of the European Bioinformatics Institution of the European Bioinformatics alicense aging the Mypothetical protein. FT COMAIN 322 332 PC FT DOMAIN 348 359 PC FT DOMAIN 369 374 PC FT DOMAIN 369 SEQUENCE 559 AA; 61652 MW; Ouery Match Best Local Similarity 100.0%; EMST Local Similarity 100.0%; EMST Local Similarity 100.0%; EMST Local Similarity 100.0%; EMST LOCAL SIMILITINIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on: June 20, 2001, 12:11:41; Search time 13.03 Seconds (without alignments) 1469.595 Million cell updates/sec Title: US-09-425-501-2 Perfect score: 559 Sequence: 1 MPLVKRNIDPRHLCHTALPRAVEYSDSEDDSEFDEVDWLE 559	table: OLIGO Gapop d: 93435 ze: 0 umber of hits sa DB seq length:	ssing ssing No.	559 100.0 559 1 Y269_HUMAN P48025 homo sapien 2

of Bioinformatics and the EMBL outstation of Bioinformatics and the EMBL outstation notitute. There are no restrictions on its lons as long as its content is in no way as not removed. Usage by and for commercial speement (See http://www.isb-sib.ch/announce/sb-sib.ch). ö trypanosoma rattus norv epstein-bar homo sapien mus musculu mus musculu gallus gall mus musculu petunia hyb homo sapien drosophila mus muscuļu Gaps KEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKQK 180 VI. by Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. K.-I., Ohira M., Kawarabayasi Y., Wiyajima-N.; Nomura N.; Nomura N.; Nomora S. Uences of unidentified human genes. W genes (KIAA0201-KIAA0280) deduced cell line KG-1 and brain."; ö 022621 p P10323 P 054804 m 098937 q 04465 m P12978 p P12978 p P42768 p P42768 p P4455 m P4455 m DB 1; Length 559; 0; Indels POLY-PRO.
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1; 44B4527BDB77BC6E CRC64; equence update) notation update) TEIN KIAA0269. 559 AA Score 559; DE Pred. No. 0; ; Mismatches ALIGNMENTS LE_PETHY
CRO_HUMAN
ICH_MOUSE
XGA_CHICK
3PT_MOUSE
IXSP_TRYBB
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MEDLINE-95127560; PubMed=7826947;
Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
"Human Fas ligand: gene structure, chromosomal location and species specificity.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fas ligand mediates activation-induced cell death in human T
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Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
TNFSF6 OR APTILG1 OR FASL.
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
PRO-NICH.
POLY-PRO.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                       Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
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--- SUBUNT: HOMOTRINER (PROBABLE).
--- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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100.0%; Pred. No. 0.00066;
ative 0; Mismatches 0;
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
NPC DERIVED PROLINE RICH PROFEIN 1 (NDPP-1).
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Wilkinson J.;
Submitted (MAY-1997) to the
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                                                                                    SEQUENCE OF 1-10 FROM N.A.
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347 TPPPPVPP---PPPPPATALQAPAVPPPPAPLQIAPGVLHP---APPPIAPPLVQPSPPV 400
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                         242 YVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPPPMHGAGDAKPIPTCISSAT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-99310608; PubMed=10381382;
MEDLINE-99310608; PubMed=10381382;
Suetsugu S., Miki H., Takenawa T.;
Suetsugu S., Miki H., Takenawa T.;
"Identification of two human WAVE/SCAR homologues as regulatory molecules which associate with the Arp2/3 Biochem. Blophys. Res. Commun. 260:296-302(1999).
EMBL; AB026543; BAA81796.1; -.
InterPro; IPR00124; -.
PinerPro; IPR00124; -.
Pfam; PF02205; WH2; 1.
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SMART; SM00246; WH2; 1.
SEQUENCE 502 AA; 55411 MW;
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MEDLINE-98402540; PubMed=9732292;
Bear J.E., Rawls J.F., Saxe C.L. III.;
BSGR, a WASP-related protein, isolated as a suppressor of receptor defects in late Dictyostellum development.";
J. Cell Biol. 142:1325-1335(1998).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                  QKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQ
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                                                                                                                                                                                                                                       338 YNPSGPPPPPPPP | : | : | : | : | : | : | 377
                                                                                                                                                                                                                                                                            SATGLIENRPQSPATGRIPVFVSPTPPPP--PPPLPSALSTSS-----LRASMIST 347
                                                                                                                                                                                                    AAEH--EYRPPS-ASARHMALNRPQQPPRRRPPQAPEGSQASAPMAPADYGMLPAQIIEY 337
                                                                                                                                                                                                                            PPPPVPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQP-SPPVARAAPV 406
                                                                                                                                                                                                                                                                CETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPH 466
                                                                                                                                                                                                                                                                                                      VPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQEAKHER 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98402540; PubMed-9732292;
Bear J.E., Rawls J.E., Saxe C.L. III.;
"SCAR, a WASP-related protein, isolated as a suppressor of receptor defects in late Dictyostelium development.";
J. Cell Biol. 142:1325-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XII
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 5:355-364(1998).
                                                                             QTYVDHMD-GSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPMHGAGDAKPIPTCIS
DTRSHASDVTDYSYPATPNHSL-------HPQPVTPSYAAGDVPPHGPASQ
                            SFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQLFDRKTLPIP
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-2099 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KIAA0900 PROTEIN (FRAGMENT).
KIAA0900.
KIAA0900.
EURATYOLA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DTEDKRKEKRKOK-OKNLDRPHEPEKVPRAPHDRRREWOKLAOGPELAEDDANLLHKHIE 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPPPSALSTSSLRASMT 345
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                               AEDIFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                     DQQLFDRKTLPIPLQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQ 167
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.
                                                                                                                                                                                                                                                                                                      89;
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EMBL/GenBank/DDBJ databases
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Last annotation update)
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; Pred. No. 1.6e-62;
42; Mismatches 154;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last and
CG4636 PROTEIN (SCAR).
                                                                                                   Pfam; PF02205; WH2; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00246; WH2; 1.
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45.8%;
Submitted (MAR-1999) to the
                  EMBL; AB020707; BAA74923.1;
EMBL; AF134305; AAD33054.1;
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                                                             InterPro; IPR002965; - InterPro; IPR003124; -
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Best Local Simil
Matches 241; C
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          RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Adril J.F., Agbayani A., An H.J., Andrews Pfannkoch C.R., Miklos G.L.G.,

RA Adril J.F., Agbayani A., An H.J., Andrews Pfannkoch C.R., Baidwin D.,

RA Adril J.F., Boyle C., Baxred E.G., Helf G., Nelson C.R., Baidwin D.,

RA Adril J.F., Boyle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,

RA Chark K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Wel M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Harris M.,

RA Harris N.L., Mattel B., Wolfnub T.J., Wel M.-H., Ibegwam C.,

RA Liu X., Mattel B., McIntob T.C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattel B., McIntob T.C., McLeod M.P., McShersin D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Blazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,

RA Sher E., Spradiling A.C., Standers R.D.C., Scheeler F., Shen H.,

RA Sher E., Spradiling A.C., Standers R., Venter E., Wang A.H., Wang Z.-Y., Wassarman D.A., Weilson M., Strong R., Saith T.,

RA Sher E., Spradiling A.C., Standers R., Venter E., Wang A.H., Wang Z.-Y., Wassarman D.A., Weilschoff M., Yang S., Yao Q.A.,

RA Jheng X.H., Zhong F.N., Zhong W., Vander J.C.,

RA Jheng X.H., Zhong F.N., Zhong W., Vander J.C.,

RY Schen R., Shen R., Shong R.N., Shong R., Shing R
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  Henderson S.N.,
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; Pred. No. 2.4e-47;
91; Mismatches 182; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of the Drosophila cytoskeletal regulator SCAR/WAVE.";
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Ashburner M.,
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32.3%;
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EMBL; AF247763; AAF74194.1;
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nterPro; IPR003124; -.
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Best Local Similarity 32.3%
Matches 218; Conservative
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SEQUENCE 613 AA;
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George R.A.,
Sutton G.G.,
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                                                                                                                                             358 SNGSGGGTPTASNANTPT-----RGRSMSTSRDAL------PPPPPVPDVISPMSGMNG 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94150718; PubMed=7906398; Milson R., Ainscough R., Anderson K., Baynes C., Berks M., Borletd J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Boritetd J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Caratton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jorer M., Johnston L., Jones M., Kershaw J., Kirsten J., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callagha M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F. Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                              ---APAVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQEAKHERIENDVATILSRRIAVEYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 GGPQQMHMQHQQMYDAGMYQSHAL-YGQTGQGVMSPEPIYGPGTPSRNKPRPSQPPPAPP
                                                                                                                                                                                                                                                                                    406 VNSGHMAAKLLGRANSSSGAGSPNSVQNANDMVMTQLSNTFHSIGMTGNQLNSLSDLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PL,PPPGIRPSSPVTVTALAHPPSGLHPTPSTAPG-----PHVPLMPPSPPSQVIPASEPK
-- ERVLVRPHEPPPPP
                                                                                                               MHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPBALSTSS----
                                                                                                                                                                                                                                                                                                                                                PPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPP
                                                                                                                                                                                                                                                                                                                                                                                                      dddddd-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PV-EEGMGSGNOHTLRPHOILPKSLANGEMOOPGOONGVPHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C7ABAD18602F590E CRC64;
                                                                                                                                                                                                                                 ----LRASMTSTPPPPPPPPPPATALQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%; Score 598; DB 5; 28.8%; Pred. No. 3.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                         ----KMSPP--NAAP----
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   -GSYSLSALPFSQMSELLTRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55349 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SED-DSEFDEVDWLE 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593 SEDSDSEDDSEGWME 607
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Pfam; PF02205; WH2; 1.
SMART; SM00246; WH2; 1
SEQUENCE 507 AA; 555
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   ----QTYVDHMD--
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                                                                                                                                                                                                                                                                                                                                                                                                      PPVPDQHSP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans."
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297 VNLDHLPPPDMSILSIDDDDDDLPPPPPPLLMNTSIVHQLPAEAPSTIQFVEPSAAPPIN 356
                                                         HSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQLFDRKTLPI 119
                                                                          120 PLQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRK 179
                                                                                                                                                                               180 KQKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRP 239
                                                                                                                                                                                                                                                                                                 300 ATGLIEN-RPQSPATGRTPVFVSPTPPPPPPPLPSAL---STSSLRASMTSTPPPPVPPP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKICNFCPFLCFPHCCPLSASFFNSRSLSDPSTTSTTTSNGYKLGCSVICSSGSKGKGAG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSGLHPT-PSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVLLEAIRKGIQ 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PPPPATALQA-----PAVPPPPAPLQIAPGVLH--PAPPPIAPPLVQPSPPVARA 403
                                                                                                                                                                                                                                                                                                                                                                                                                     404 APVCETVPV----HPLPQG----EVQGLPPPPPPPPPPPGIRPSSPVTVTA----LAHP 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Saxe C.L., Bear J.E., Rawls J.F.;
"SCAR, a WASP-related protein, isolated as a suppressor of receptor defects in late Dictyostellum development.";
Cell Biol, Int. 143:1325-1335(1998).
EMBL; AF079805; AAD29083.1; -.
                                                                                                                                                                                                                                          QTYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPPMHGAGDAKPIPTCISS
MPLVKRNIDPRHLCHTALPRGI-KNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEA
               202 TAYNDMQHRNRQISGSRINQQNEVFSFPEE-----YQAP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 LRKVEEQREQEAKHERIE-NDVATILSRRI--AVEYSDSEDDSEFDEVDW 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48389 MW; CAA05B0A790454F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum
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Last annotation update)
                                                                                                                                                                                                          ----RVKSPNDGSKSPKKRRKQ---PGQGP-----
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PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00246; WH2; 1.
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Q9XYA8;
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478 V-IPASEPKRHPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQEAKHERIENDVATILS 536
                                                                         60 HSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITM--RKAFRSSTIQDQQLFDRKTL 117
                                                                                                   NUVTQRIEKLGSRIRPLIQSIPSIEDYHRNTSIDTMNSKPRAEFHADNSERNQHFTHASI 121
                                                                                                                                                PIPLQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKR 177
                                                                                                                                                                     KOKOKNLDRPHEPEKVPRAPHDRRREWOKLAQGPELAEDDANLLHKHIEVANGPASHFET 237
                                                                                                                                                                                                                                                                                                  RPQTYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPPMHGAGDAKPIPTCI 297
                                                                                                                                                                                                                                                                                                                                                                         SSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPLPSALSTSSLRASMTSTPPPPPPPPPPPP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                PPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQ 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --IVGAPAPPPPPP-----PPPS------PPS-----PPPPMAK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 AGGASDIK------PKASGARSDLLSSIMQGMALKPAEERKVAEAPKKEEALNVADILA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Bugonliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
MPLVKRNIDPRHLCHTALPRGIKNEL-ECVTNISLANIIRQLSSLSKYAEDIFGELFNEA
                                  LPSVTDNNQP-----ALEGQSKDQIVDTVITSTTVGIINQLTMLVAHSNSIFTALANDA
                                                                                                                                                                                                                                                           ERREARLKKKGEKNEV---EVKKVKSVTKVRYDPVTGE------KITINIESPHTS
                                                                                                                                                                                                                                                                                                                       | | : | : | SPQ--IQHQSNN---TATP------QHTTQHEGTNQYQAPPPPPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPSTGFN---TPPPPMSNN-----NNMPPP--PPMQQNGGAANNRLSVHNSAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEVOGLPPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 348-747 FROM N.A. Cobben J., Grymonprez B., Volckaert G, Mewes H.W., Lemcke Mayer K.F.X.; F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
EXTENSIN-LIKE PROPEIN.
19E8.80 OR AT4G13340.
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Submitted (MAR-2000)
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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15.1%; Score 449; DB 5; Length 443; 26.7%; Pred. No. 4.4e-23; Live 75; Mismatches 205; Indels 132;

Best_Local Similarity 26.73 Matches 150; Conservative

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Query Match

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                         85;
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MOD_RES
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                         Matches
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P70433
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                                                                                                                                                                                                                                   272 LVRPHEPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPL 331
                                                                                                                                                                                                                                                        332 PSALSTSSLRASMISTPPPPPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAP 391
                                                                                                                                                                                                                                                                                                   507
                                                                                                                                                                                                                                                                                                                         451
                                                                                                                                                                                                                                                                                                                                      52; Gaps
                                                                                                                                                                                                                                                                                          392 PLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPPGIRPSSPVTVTALAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Volvox carteri f. nagariensis.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae; Volvox.
NCBI_TaxID=3068;
                                                                                                                                                                                                                                                                                                                                                                                  452 PSGLHPTPSTAPGPHVP-----LMPPSPPSQVIPASEPKRHPSTLPVIS: 495
                                                                                                                                                                                        Length 760;
                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL049608; CAB40769.1;
EMBL; AL161536; CAB78376.1;
InterPro; IPR00151;
InterPro; IPR002955;
InterPro; IPR002955;
InterPro; IPR002965;
InterPro; IPR002965;
InterPro; IPR002965;
Pfam; PF00560; LRR; 2.
PRINTS; PR01211; PR1HEXTENSN.
PRINTS; PR01211; PR1HEXTENSN.
PRINTS; PR012118; PSTLEXTENSIN.
                                                                                                                                                                                                              Indels
                                                                                                                                                         20CDE1C8E6CEECFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.
                                                                                                                                                                                        Query Match 12.2%; Score 363; DB 10; 1
Best Local Similarity 36.4%; Pred. No. 5.7e-17;
Matches 84; Conservative 13; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                409 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HK10;
MEDLINE=20044763; PubMed=10574980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO1218; PSTLEXTENSIN.
PRINTS; PRO0239; RHODOPSNTAIL.
                                                                                                                                                       760 AA; 82245 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                           SMART; SM00370; LRR;
SEQUENCE 760 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
18 4
409 AA;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9SBM1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               09SBM1
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
Q9SBM1
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-!- ALTERNATIVE PRODUCTS: FOUR FORMS; MENA+, MENA+, AND MENA++
(SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
EMBL; U72520; AAC52864.1; -.
EMBL; U72521; AAC52866.1; -.
EMBL; U72522; AAC52866.1; -.
EMBL; U72522; AAC52866.1; -.
INTERPROSITED BY ALTERNATIVE SPLICING.
INTERPROSITED BY ALTERNATIVE SPLICING.
InterProsite By AAC52866.1; -.
InterProsite By AAC52866.1; -.
InterProsite By AAC52866.1; -.
InterProsite By AAC52866.1; -.
                                                                      275 PHEPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPA 334
                                                                                                       335 LSTSSLRASMTSTPPPPPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLV 394
                                                                                                                   395 QPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSSPVTVTALAHPPSG 454
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-ARG.
PHOSPHORYLATION (BY CAPK AND CGPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGPK) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
MISSING (IN ISOFORM MENA+).
MISSING (IN ISOFORMS MENA AND MENA+).
CIFC -> VFYL (IN ISOFORM MENA++).
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                               31;
        Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
PHOSPHORYLATION (BY CAPK AND
Score 358.5; DB 10; Lews-Pred. No. 6e-17;
                                                                                                                                                                                                     455 LHPT---PSTAPGPHVPLMP---PSPPSQVIPASEPKRHPSTLP 492
                                                                                                                                                                                                                    P70433: P70430: P70431: P70432: 01. FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) ENABLED HOMOLOG.
                                                                                                                                                                                                                                                                                        802 AA
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POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation
                                                                                                                                                                                                                                                                                       PRT;
                                 6
        12.0%;
                                 Conservative.
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00568; WH1; 1.
SMART; SM00160; RanBD;
Alternative splicing; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131
135
135
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117
132
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-LHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRP- 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SSPVTVTALAHPPSGLHPTPSTAPGPHVPL-MPPS----PPSQVIPASEPKRHPSTLP 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 PHEPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPA--TGRTPVFVSPTPPPPPLP 332
                                                                                                                                                                                                                                                                                                                                                118 PPSPPSPAPPSPSPPAPPSPSPAPPL....PPSPAPPSPSPSPVPPSPAPPSPAP 173
                                                                                                                                                                                                                                                                                                                                                                                                 333 SALSTSSLRASMTSTPPPPPPPPPPPATALQAPAVPPPPAPLQIAPGV------ 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 YNSPRGYFHTFAGDTCQVALNFANEEEAKKFRKAVTDLLGRRQRKSEKRRDPPNGPNLPM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---HDRRREWQKLAQGPELAEDD----ANLLHKHIEVAN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 YTNPSYFFDLWKEKMLQ-----DTEDKRKEKRK-----QKQKNLDRPHEPEKVPRAP- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 161; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostom1;
                                                                                                                                                                                                 11.9%; Score 354.5; DB 10; Length 555; 38.3%; Pred. No. 1.6e-16; Live 14; Mismatches 95; Indels 39;
     Goodenough U.W.;
"Glycosylated polyproline II rods-with-kinks as a structural plant hydroxyproline-rich glycoproteins.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF309494; AAG45420.1; -
SEQUENCE 555 AA; 54219 MW; 6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rat brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 GPASHFETRPQTYVD-----HMDGSYSLSALPFSQMSELLTRAEERVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54824 MW; BC5670A11AB63539 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04, Created)
04, Last sequence update)
16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97464048; PubMed=9322739;
Fukuoka M., Miki H., Takenawa T.;
"Identification of N-MASP homologs in human and
Gene 196:43-48(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 350.5; DB 4 25.5%; Pred. No. 2.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D88460; BAA20128.1;
InterPro; IPR000095; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001960; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00568; WH1; 1
Pfam; PF00786; PBD; 1
Pfam; PF02205; WH2; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00246; WHZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000697
                                                                                                                                                                                                                             Best_Local Similarity
Matches 92, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM
SEQUENCE
                                                                                                                                                                                                      Query Match
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                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: | : | : | : | : | : | : | ALEVLNSQEAAQSKVTATQDSTNLRCIFCGPTLPRQNSQLPAQVQNGPSQEELEIQRRQL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 PPPPPPDLPNQAPPP-----PPPPPAPPLPAS------GIFSGSTSEDNRPLTGLA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----RERLERERLEGEQUERQRQEREHVERLERERLERERGERERERLEGLEREQVE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HFETRPQTYVDHMDGSYSLSALPFSQMSE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 PPTSTPPTPPLRHAATRFATSLGSAFHPVLPHYATVPRPLNKNSRPSSPVNT-PSSQPPA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TPVFVSPT-----PPPPPPPPLPSALSTSSLRASMTSTPPPPPPPPPPATALQ- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------PPPGIRPSSPVTVTALA 449
                                                                                                                                                                                                                                                                                                                                                                                              RKAFRSSTIQDQQLFDRKTLPIPLQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WERERRMSNAAPSSDSSLSSAPLPEYSSCOPPSAPPPSYAKVISAPVSDATPDYAVVTAL 307
                                                                                                                                                                                                 3 LVKRNI-DPRHLCHTALPRGIKNELECVTNISLANIIRQLSSL---SKYAEDIFG---- 53
                                                                                                                                                                                                                                                                                                  --ELFNEAHSFSFRVNSLQERVDRLSV------SVTQLDPKEEELSLQDITM 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDLWKEKMLQD-TEDKRKEKRKQKQKNLDRPHEP--EKVPRAPHDRRR------E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 EPGLQAASQPAESPTPQGLVLGPPAPPPPPPPLPSGPAYASALPPPPGPPPPPLPSTGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                            ------RERLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 LLTRAEERVLVRPHEPPPP----PPMHGAGDAKPIPTCISSATGLIENRPQSPATGR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --APAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARS-----VLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
                                                                                              12.0%; Score 356.5; DB 11; Length 802; 22.5%; Pred. No. 1.7e-16; tive 83; Mismatches 196; Indels 241;
     500 MISSING (IN ISOFORM MENA)
85844 MW; 592BB975EE20F77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
VEGETATIVE CELL WALL PROTEIN GP1.
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OEOOROKELERERM-ERERLE------
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                                                                                                                                                   Matches 151; Conservative
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MEDLINE-92289669; Pubmed-1600938;
Ettl H., Hallmann A., Wenzl S., Sumper M.;
A novel extensin that may organize extracellular matrix biogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 PATG-RTPVFVSPTPPP----PPPPLPSALSTSSLRASMTSTPPPPVPP-----PPPPPA 360
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--IGHVGWDPNTGSDLNNLDPELKNLFDMCGILEAQLKE---RETLKVIYDFIEKTGGVE 266
                                                             316 RAPTAAPPPPPSS------RPSVEVPPPPPNRMYPPPPPALPSSAPSGPPPPPSVLGV 368
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------pppppgppppgL-- 391
                                                                                                                                                                                                      380 GVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPGIRP 439
                                                                                                                                                                                                                                                                                     440 SSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKR-HPSTLPVISDAR 498
                                                                                                                                                                                                                                                                                                                                                                                            -----PPPPLPSALSTSSLRASMTSTPPPPVPP-PPPPPATALQAPAVPPPPAPLQIAP 379
                                                                                                                                                                                                                                                                                                                                                                    499 SVLLEAIRKGIQLRKVEEQREQ----EAKHERIENDVATILSRRIAVEYSDSEDDSEFDE 554
                                                                                                                                                                                                                                                                                                               ----VRPHEPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPP-
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Sukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Volvocaceae: Volvox.
NCBI_TaxID=3067;
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11.7%; Score 348.5; DB 10; Length 464;
Best Local Similarity 37.0%; Pred. No. 3.3e-16;
Matches 90; Conservative 19; Mismatches 89; Indels 45;
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Last annotation update)
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Mendel; 17416; Volca;2658;17416.
InterPro; IPR000480; -.
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PRINTS; PRO1217; PRICHEXTENSN.
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SEQUENCE 464 AA; 47838 MW;
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01-OCT-2000 (TrEMBLrel.
EXTENSIN (FRAGMENT).
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                                                                                                                                                                                                                                          369 GPVAPPPPP----
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065553 bovine herp 061078 mus musculu 09p2r6 homo sapien

Run on:

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MEDILNE=20428428; Pubmed=10970852; WEStDHAIR R.S., Scott J.D.; Westphal R.S., Soderling S.H., Alto N.M., Langeberg L.K., Scott J.D.; Westphal R.S., Soderling S.H., Alto N.M., Langeberg L.K., Scott J.D.; Scarf/WAVE-1, a wiskott-aldrich syndrome protein, assembles an actinassociated multi-kinase scaffold."; EMBO J. 19:4589-4600(2000). BEMBL: AFSUGNIT; ARGO2214.1; SEQUENCE 559 AA; 61508 MW; 8746910987DB0D16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2942; DB 11; Length 559;
Pred. No. 5e-193;
3; Mismatches 6; Indels 0
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Last annotation update)
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Q9NGX1
Q9LMQ1
Q9VZC2
Q9XDH2
Q9LT74
Q6LT74
Q62775
                                       Q9VAY4
Q9DEH3
Q9SPM0
Q36027
Q41805
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O48809
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Q62901
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
1012
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1566
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                                                                                            June 20, 2001, 12:07:11 ; Search time 37.19 Seconds (without alignments) 1988.667 Million cell updates/sec
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1 MPLVKRNIDPRHLCHTALPR......AVEYSDSEDDSEFDEVDWLE
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q9T0K5
Q9SBM1
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Gapop 10.0 , Gapext 0.5
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Q9UDY7
Q9UPY6
094974
Q9VKM2
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sp_vertebrate:*
sp_virus:*
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sp_mammal:*
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sp_bacteria:*
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sp_plant:*
sp_rodent:*
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Maximum DB seq length: 2000000000
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OKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQ

121 LQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKQK 180

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P70433 Q9FPQ6 O00401

112 113 113 114 118 118

Result No.

Q41645 Q9SPM1 Q9XIL9 Q08816

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LQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKQK 180
                  QKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQ 240
                                                                                      352 VPP---PPPPPATALQAPAVPPPPAPLQIAPGVLHP---APPPIAPPLVQPSPPVARAAP 405
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                                                                                                                                                                                                          PTCISSATGLIENRPQSPATG - - RTPVFVSPTPPPPPPPPPRASALSTSSLRASMTSTPPPP 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEWBLrel. 07, Created)
01-AUG-1998 (TrEWBLrel. 07, Last sequence update)
01-MAR-2001 (TrEWBLrel. 16, Last annotation update)
DJ393P12.2 (HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 LIKE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases: EMBL; AA.022578; CAA.18609.1; -. InterPro: IRR03124; -. Pfam: PF02205; WH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497 AA; 54062 MW; 58872599FDF63A6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 1199; DB 4; 47.6%; Pred. No. 3.4e-74; Live 52; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 DVVGNDVATILSRRIAVEYSDSEDDSSEFDEDDW 496
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Best Local Similarity 47.6%
Matches 276; Conservative
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SEQUENCE
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                                                                                      TALQAPAVPPPAPLQIAPGVHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEV 420
                                                                                                                                                                                                                            TALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEV 420
                                                                                                                                                                                                          QGLPPPPPPPPPPLPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIP 480
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                                                                                                                                                                                                                                                                                              1 MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEAH 60
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.3%; Score 1259.5; DB 4; Length 498; 50.5%; Pred. No. 2.6e-78; ive 51; Mismatches 138; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              general complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
Hall R.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB0J6542; BAA81795.1; -.
EMBL; AL096774; CAC18518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C737CE963016DE94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99310608; PubMed-10381382;
Suetsugu S., Miki H., Takenawa T.;
"Identification of two human WAVE/SCAR homologues as regulatory molecules which associate with the Arp2/3 Biochem. Biophys. Res. Commun. 260:296-302(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAY-2001 (TrEMBLrel. 16, Last annotation update)
WASP-FAMILY PROTEIN (DJ144C9.2).
WAVEZ OR DJ144C9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 AA
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003124; -- Pfam; PF02205; WH2; -- Pfam; PR02205; WH2; PRICHEXTENSIN, PRINTS; PR012118; PSTLEXTENSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498 AA; 54283 MW;
                                                                                                                                                                                                                                                                                                                                                               541 VEYSDSEDDSEFDEVDWLE 559
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Best Local Similarity
Matches 290; Conserv
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34756 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01088; CAP_1; 1. PROSITE; PS01089; CAP_2; 1. Membrane; Multigene family.
EMBL, D13634; BAA02798.1;
Hypothetical protein.
DOMAIN 165 178
SEQUENCE 314 AA; 34756
                                                                                                                                         Query Match 2.0°
Best Local Similarity 100°
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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Pfam; PF01213; CAP;
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15-JUL-1998 (
01-OCT-2000 (
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Q15032;
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CAP2_HUMAN
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifiad and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Buropean Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                              Sazuka T., Tomooka Y., Kathju S., Ikawa Y., Noda M., Kumar S.;
"Identification of a developmentally regulated gene in the mouse
central nervous system which encodes a novel proline rich protein.",
elochim. Blophys. Acta 1132:240-248(1992).
-!- FUNCTION: MAY PLAY AN IMPORTANT BIOLOGICAL ROLE IN THE
DEVELOPMENT AND DIFFERENTIATION OF THE CENTRAL NERVOUS SYSTEM.
-!- TISSUE SPECIFICITY: IN THE HEART AND TESTIS AND LESS SO IN THE
LUNG, SKELETAL MUSCLE, KIDNEY, PANCREAS AND BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y., Sato S., Nagase T., Seki N., Ishikawa K. I., Tabata S., Prediction of the coding sequences of unidentified human genes I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EE36C1CBE8156033 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-CCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN KIARO009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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MEDLINE-96051387; PubMed-7584026;
                                                                                           MEDLINE-93041923; PubMed-1420303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41249 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D10727; BAA01570.1; -.
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195
276
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Developmental protein
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Best Local Similarity
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    NCBI_TaxID=10090;
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Q15390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-95051124; PubMed-7962207; Yu G., Swiston J., Young D.; "Comparison of human CAP and CAP2, homologs of the yeast adenylyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                            Length 314;
                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2FD3950C094F5AF7 CRC64;
POLY-PRO.
E79E4F4E310619E3 CRC64;
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                                                                                                         2.0%; Score 11; DB 1; 100.0%; Pred. No. 0.0069; iive 0; Mismatches 0
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
ADENYLYL CYCLASE-ASSOCIATED PROTEIN 2 (CAP 2)
                                                                                                                                                                                                                                                                                                                                                                                                                         477 AA.
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SIMILARITY: CONTAINS 2 CBS DOMAINS
                                                                                                                                            PIR; S19595;
                                                                                                                                                                                                                                                             domain.
                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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NO20_SOYBN
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                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                        une European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                           Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y., Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.; Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIRAMO01-KIRAMO040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: VOLTÂGE-GÂTED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
TRANSEPITHELIAL TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CHLORIDE CHANNEL PROTEIN, SKELETAL MUSCLE (CHLORIDE CHANNEL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN SKELETAL MUSCLES.
SIMILARITY: TO OTHER CHLORIDE CHANNELS.
            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Skeletal muscle;
MEDLINE-92065954; PubMed-1659664;
Stalnmeyer K., Ortland C., Jentsch T.J.;
Frimary structure and functional expression of a developmentally regulated skeletal muscle chloride channel.";
Nature 354:301-304(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0%; Score 11; DB 1; Length 971;
100.0%; Pred. No. 0.02;
iive 0; Mismatches 0; Indels
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POLY-PRO.
1; D07684D368955108 CRC64;
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                                                                                                   TISSUE-Bone marrow;
MEDLINE-96051387; PubMed-7584026;
                                                                                                                                                                                                                                                                                                                                                                                                                  107673 MW;
HYPOTHETICAL PROTEIN KIAA0029
                                                                                                                                                                                                                                                                                                                                       EMBL; D21852; BAA04878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                             cell line KG-1.";
DNA Res. 1:27-35(1994).
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001374; -
Pfam; PF01424; R3H; 1.
Hypothetical protein.
DOMAIN 461 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 PPPPPPPLPP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 PPPPPPPLPP 434
                                                                                                                                                                                                                                                                                                                                                                                                                 971 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLC1_RAT
P35524;
01-JUN-1994 (
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                                                  modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
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01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Glycine max (Soybean).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Pabales; Pabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                         [onic channel; Ion transport; Voltage-gated channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandal N.N., Bojsen K., Marcker K.A.;
"A small family of nodule specific genes from soybean.";
Nucleic Acids Res. 15:1507-1519(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCDDCD0D26E48FAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
CBS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
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100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (POTENTIAL).
2 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
9 (POTENTIAL).
9 (POTENTIAL).
10 (POTENTIAL).
11 (POTENTIAL).
12 (POTENTIAL).
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SEQUENCE FROM N.A. (TRUNCATED FORM N-20T).
STRAIN-CV. DARE; TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-87146477; PubMed-3822835;
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0
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                                                                                                                                                                                                                                                                        InterPro; IPR002243; -. Pfam; PF00571; CBS; 2. Pfam; PF00654; voltage_CLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                    EMBL; X62894; CAA44683.1; -.
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00762; CLCHANNEL.
PRINTS; PR01112; CLCHANNEL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                              InterPro; IPR000644; -. InterPro; IPR001807; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 PPPPPPPLPP 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                   EACH INCLUDING TWO CYC-7AA-CYS ARRANGEMENTS ARE METAL-BINDING DOMAINS. ANALOGOUS TO THE 'FINGER REGIONS' PRESENT IN METAL-BINDING PROTEINS; THE BINDING OF METAL IONS SEEMS TO BE IMPORTANT FOR THE FUNCTION OF THESE NODILINS. SIMILARITY: TO NODULIN 22, 23 AND 44 AND PARTIAL TO METAL-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO NODULIN 22, 23, 44 AND TO THE 'FINGER REGIONS' OF METAL-BINDING PROTEINS.
TO NODULIN 22, 23, 44 AND TO THE 'FINGER REGIONS' OF METAL-BINDING PROTEINS.
MISSING (IN TRUNCATED FORM N-20T).
94F21F90B68A6CA2 CRC64;
                              Sengupta-Gopalan C.;
on of a highly expressed late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownken R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                    -! - MISCELLANEOUS: THE AUTHORS SUGGEST THAT THE 2 CONSERVED DOMAINS
                                                                                                                         Mol. Gen. Genet. 229:445-452(1991).
-1- SUBCELLULAR LOCATION: PERIBACTEROID MEMBRANE OR PERIBACTEROID
                                                                                                                                                                                         SPACE (POTENTIAL).
-!- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM
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0. 0.039;
0; Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL 23.6 KDA PROTEIN T23G5.3 IN CHROMOSOME III.
                           Richter H.E., Sandal N.N., Marcker K.A., Sengu
"Characterization and genomic organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 10; 100.0%; Pred. No.
                                                                                              nodulin gene subfamily in soybeans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B26669; B26669.
Nodulation; Signal; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
MEDLINE-94150718; Pubmed-7906398;
PubMed=1840639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20022 MW;
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Best Local Similarity 100.C
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 LPPPPPPPL 432
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                                                                                                                                                                                                                                                             INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEINS
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NA PRESENTATION OF THE PRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Inactivation of the survival motor neuron gene, a candidate gene for human spinal muscular atrophy, leads to massive cell death in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 94:9920-9925(1997).
-!- FUNCTION: THE SMN COMPLEX PLAYS AN ESSENTIAL ROLE IN SPLICEOSOMAL.
SNRNP ASSEMBLY IN THE CYTOPLASM, AND IS REQUIRED FOR PRE-MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDIATE-9724505; PubMed=9070939; MEDIATE-97224505; PubMed=9070939; Viollet L., Bertrandy S., Brunialti A.L.B., Lefebvre S., Burlet P., Clermont O., Cruaud C., Guenet J.-L., Munnich A., Melki J.; "cDMA isolation, expression, and chromosomal localization of the mouse survival motor neuron gene (Smn)."; Genomics 40:185-188(1997).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                        "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97264340; PubMed-9110173;
Didonato C.J., Chen X.N., Noya D., Korenberg J.R., Nadeau J.H.,
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             Vaudin M., Vaughan K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 211;
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughar
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10; DB 1; Length Lizer Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 protein.
211 AA; 23552 MW; 85D829BEDEA17740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMN_MOUSE STANDARD; PRT; 288 AA. P97801; 009092; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update) SURVIVAL MOTOR NEURON PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-97420785; PubMed-9275227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z19158; CAA79571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Senome Res. 7:339-352(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S28304; S28304.
WormPep; T23G5.3; CE00333.
                                                                                                                                                                          Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse)
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SEQUENCE 21
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                                                                                                                                                  elegans
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SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE P53 FAMILY.

SUBCELLULAR LOCATION: NUCLEAR

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SPLICING IN THE NUCLEUS (BY SIMILARITY).
SUBUNIT: FORMS A STABLE HETEROMERIC COMPLEX WITH SURVIVAL OF MOTOR
BUBINON PROTEIN INTERACTING PROTEIN 1 (SIPI/GEMIN3), GEMIN3 AND
GEMINA, THIS COMPLEX IS THOUGHT TO PLAY AN ESSENTIAL ROLE IN
BIOGENESIS OF THE SMALL NUCLEAR RIBONUCLEOPROPEIN PARTICLES
                                                                                                          (SNRNPS). INTERACTS WITH FIBRILLEARIN AND WITH SEVERAL SPLICEOSOMAL SNRNP CORE SM PROTEINS, INCLUDING B/B', SM D AND SM E PROTEINS (BY
                                                                                                                                                                                                   WHICH
                                                                                                                                                                         SUBCELLULAR LOCATION: CYTOPLAMIC AND NUCLEAR. LOCALIZED IN SUBNUCLEAR STRUCTURED NEXT TO COILED BODIES, CALLED GENS, WH ARE HIGHLY ENRICHED IN SPLICEOSOMAL SNRNPS (BY SIMILARITY). SIMILARITY: BELONGS TO THE SMN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 757B3074649F7458 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:109257; Smn.
mRNA processing; RNA-binding; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY - PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 AA; 31254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U63294; AAC53057.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAA73356.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196
                                                                                                                                                       SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Gaps ; 0 1.8%; Score 10; DB 1; Length 288; 0; Indels 0.06; 100.0%; Pred. wo Query Match 1.8 Best Local Similarity 100. Matches 10; Conservative 426 PPPPPPLPPP 435 111111111 212 PPPPPLPPP 221 ð 合

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NUCLEIC ACIGS Res. 16:11383-11383(1988).

-! FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTTVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANSACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED BITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear 01-MAR-1989 (Rel. 10, Created)
1-MAR-1989 (Rel. 10, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53). 367 AA PRT; STRAIN-SPAFAS; MEDLINE-89083584; PubMed-3060861; STANDARD; Gallus gallus (Chicken) SEQUENCE FROM N.A. NCBI_TaxID-9031; oncoprotein. P53_CHICK P10360; Soussi T.; Gallus. P53_CHICK

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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                        EMBL outstation
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PHOSPHORYLATION (BY SIMILARITY).
FC37D0FCDF9195B6 CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96096534; PubMed-8522189;
MEDLINE-96096534; PubMed-8522189;
Medel 3. (Aubbersteey A., Yu G., Young D.;

"Differential expression of CAP and CAP2 in adult rat tissues.";

Gene 165:273-277(1995).

-i - FUNCATION: MAY HAVE A REGULATORY BIFUNCTIONAL ROLE.

-i - FUNCATION: MAY HAVE A REGULATORY BIFUNCATIONAL ROLE.

-i - TISSUE SPECIFICITY: FOUND AT RELATIVELY HIGH LEVELS IN TESTES,

MODERATE LEVELS IN BRAIN, HEART AND SKELETAL MUSCLE, AT LOWER

LEVELS IN LUNG, SKIN, KIDNEY AND SMALL INTESTINE, AND IS

UNDETECTABLE IN LIVER OR SPILEEN.
                                                                                                                                                                                                                                                                                                        PRINTS; PR00366; P53SUPPRESSR.
PROSITE; PS00348; P53; 1.
Anti-oncogene; DNA-binding; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                             Nuclear protein; Phosphorylation; Apoptosis.

1 30 TRANSCRIPTION ACTIVATION (ACIDIC).

DNA_BIND 87 278 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                               OLIGOMERIZATION.
BASIC (REPRESSION OF DNA-BINDING)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 367;
                                                                                        the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 0.075;
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01-0c7-1996 (Rel. 34, Last sequence update)
01-0c7-1996 (Rel. 34, Last annotation update)
BENILYL CYCLASE-ASSOCIATED PROTEIN 2 (CAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 AA
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W.
                                                                                                                                                                                                                EMBL; X13057; CAA31456.1; -. PIR; S02193; S02193.
HSSP; P04637; 1TSR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   292
366
367 AA;
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50 PPPPPPPLP 59
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Best Local Simi
Matches 10;
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P52481;
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2D7E82A953B1339E CRC64;

60243 MW;

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551 AA;
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                                                                                                                                                                          CN4D_HUMAN
SEQUENCE
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                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawamukai M., Gerst J., Field J., Riggs M., Rodgers L., Wigler M.,
                                                                                                                                                             ;
0
                                                                                                                                  DB 1; Length 477;
0.096;
hes 0; Indels
                                                                                                CFCD65E8F256655B CRC64;
                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schigosaccharomycetales; Schizosaccharomycetaceae;
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POLY-PRO.
                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                         551 AA
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                     ADENYLYL CYCLASE-ASSOCIATED PROTEIN (CAP).
                                                                                                                                   1.8%; Score 10;
100.0%; Pred. No.
                                                                                      POLY - PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MK141;
MEDLINE=92199347; PubMed=1550959;
                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
30-MAY-2000 (Rel. 39, Last anno
                                                                                               52912 MW;
                   InterPro; IPR001837; -. Pfam; PF01213; CAP; 1. PR0SITE; PS01088; CAP_1; 1. PR0SITE; PS01089; CAP_2; 1. Membrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL049728; CAB41657.1;
PIR; A60047; A60047.
InterPro; IPR001837; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01088; CAP_1; 1. PROSITE; PS01089; CAP_2; 1. Membrane.
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           U31935; AAA92298.1;
                                                                                                                                 Ouery Match 1.89
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                 111111111
231 GLPPPPPPP 240
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                                                                                                477 AA;
                                                                                                                                                                                    422 GLPPPPPPP 431
                                                                                                                                                                                                                                                                                                                                                CAP OR SPCC306,09C
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
306
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=972;
                                                                                                                                                                                                                                                           CAP_SCHPO
ID CAP_SCHPO
AC P36621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young D.;
                                                                                                SEQUENCE
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 S T W D R R D R F S
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: WIDESPREAD; MOST ABUNDANT IN SKELETAL MUSCLE. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baecker P.A., Obernolte R., Bach C., Yee C., Shelton E.R.; "Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiesterase (PDE IVD)."; Gene 138:253-256(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF THE PROTEIN ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (FORMS 4/HPDE4D1; 5/HPDE4D2 AND 2/HPDE4D3).
MEDLINE=96390839; PubMed=8797812;
Nemoz G., Zhang R.B., Sette C., Conti M.;
"Identification of cyclic AMP-phosphodiesterase variants from the PDE4D gene expressed in human peripheral mononuclear cells.";
FEBS Lett. 384:97-102(1996).
-:- CATALYTY: AMP-DENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)0 = ADENOSINE 5'-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ALL FORMS), AND REVISIONS TO FORM 2/HPDE4D4. MEDLINE-98041897; Pubmed-9371713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        learning and memory gene product of Drosophila melanogaster are potential targets for antidepressant drugs."; Mol. Cell. Biol. 13:6558-6571(1993).
                                                                                                                                                                                                                                        008499; Q13549; Q13550; Q13551; O43433;
01-0CT-1996 (Rel. 34, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4D (EC 3.1.4.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolger G.B., Erdogan S., Jones R.E., Loughney K., Scotland G., Hoffmann R., Wilkinson I., Farrell C., Houslay M.D.; "Characterization of five different proteins produced by alternatively spliced mRNAs from the human cAMP-specific
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94019330; PubMed-8413254;
Bolger G., Michaell T., Martins T., John T., Steiner B.,
Rodgers L., Riggs M., Wigler M., Perguson K.;
"A family of human phosphodiesterases homologous to the dunce
Length 551;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (FORMS 1/HPDE4D3 AND 2/HPDE4D4)
    DB 1;
0.11;
                                                                                                                                                                                                                          809 AA.
  1.8%; Score 10; DB 100.0%; Pred. No. 0.1; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: INHIBITED BY
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94171048; PubMed=8125310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphodiesterase PDE4D gene.";
Biochem. J. 328:539-548(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (FORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY ALTERNATIVE SPLICING
  Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                            STANDARD;
                                                                               422 GLPPPPPPPP 431
                                                                                                      111111111
304 GLPPPPPPP 313
                                                                                                                                                                                                                                                                                                                                               (DPDE3) (PDE43).
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SEQUENCE OF 468-853 FROM N.A. (ISOFORMS 1 AND 2).
           Smith M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
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DOMAIN
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          (See http://www.isb-sib.ch/announce/
                                                                                                                                                   TSTAVETGHRPGLKKSRMSWPSSFQGLRRFDVDNGTSAGRS
PLDPMTSPGSGLILQANFVHSQRRESFLYRSDSDVDLSPKS
BRNSSIASDLLIVPTPRQVLASLRTVRNNFAALTNL
QDRAFSKRSPMCNQPSINKATIT -> MKGPSCAGTGHPM
AGYGRMAPFELASGPVKRLRTESPFPCLFA (IN
                                                                                                                                                                                                               (IN ISOFORM 6/HPDE4D5)

BABEGSSAPARAGSGESCBSAGGATLKAPKHLWRHEQHHQY
PLRQPOFRLLHPHHLLPPPPPSPQPQPQCPCCPLQPPPPPPLP
PPPPPPGAARGRYASSGATGRVRHGYSDTERYLYCRAMDR
PSYAVETGHPROELKE REMSWPSSFQCLRR -> MMHVNNFF
RRHSMIC (IN ISOFORM 1/HPDE4D3).
MISSING (IN ISOFORM 3).
                                                                                                                                                                                                                                                                                 MEAEGSSAPARAGSGEGSDSAGGATLKAPKHLWRHEQHHQY
PLRQPQFRLLHPHHLJPPPPPSPQPQPQCPLQPPPPPPLP
PPPPPGAARGRYASSGATGRVRHRGYSDTERYLYCRAMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DIAPHANOUS PROTEIN HOMOLOG 3 (DIAPHANOUS-RELATED FORMIN 3) (DRF3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
[2]
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                                                                                                                                                                                                                                                                                                                                                            ISOFORM 4/HPDE4D1).
MISSING (IN ISOFORM 5/HPDE4D2)
R -> P (IN REF. 3).
C -> R (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 7A4773DD3A044F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
         entities requires a license agreement (
    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.8%; Soc
Best Local Similarity 100.0%; P:
Matches 10; Conservative 0;
                                              120969; AACOO042,1; -. 102882; AACI3745.1; -. 1050157; AAG13745.1; -. 1050158; AAG97890.1; -. 1050159; AAG97892.1; -. AEC012074; AACOO069.1; -. AEC12073; AACOO069.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                  Pfam; PF00233; PDBase; 1.
PRINTS; PR00387; PDIESTERASE1.
PROSITE; PS00126; PDEASE_1; 1.
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                                     EMBL; L20970; AAA03592.1; -.
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                                                                                                                                                                                                                          152
                                                                                                                           InterPro; IPR002073;
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644
769
7809 AA;
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DIAPH3 OR DIAP3.
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                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                        VARSPLIC
VARSPLIC
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EMBL;
EMBL;
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                                                                                                                                                                                                                                    SIMILARITY).

-I-ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-I-DOMAIN: DRFS ARE REGULATED BY INTRAMOLECULAR GBD-DAD BINDING WHERE RHO-GTP ACTIVATES THE DRFS BY DISRUPTING THE GBD-DAD INTERACTION (BY SIMILARITY: CONTAINS I GTPASE-BINDING DOMAIN (GBD).
-I-SIMILARITY: CONTAINS I FORMIN HOMOLOGY 2 (FH1) DOMAIN.
-I-SIMILARITY: CONTAINS I FORMIN HOMOLOGY 2 (FH2) DOMAIN.
-I-SIMILARITY: CONTAINS I FORMIN HOMOLOGY 3 (FH3) DOMAIN.
-I-SIMILARITY: CONTAINS I FORMIN HOMOLOGY 3 (FH3) DOMAIN.
-I-SIMILARITY: CONTAINS I FORMIN HOMOLOGY PAMILY. DIAPHANOUS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARG/LYS-RICH (BASIC).
VSVETLEKNLRQMGRQLQQLEKELETFPPPEDLHDKFVTKI
F -> GLCLFKKHFMALIFSAKRLKIIPFICMYFPLSHSVF
SUBMITTER (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS TO GTP-BOUND FORM OF RHO AND TO PROFILIN. ACTS IN A RHO-DEPENDENT MANNER TO RECRUIT PROFILIN TO THE MEMBRANE, WHERE IT PROMODES ACTIN POLYMERIZATION. IT IS REQUIRED FOR CYTOKINESIS, STRESS FIBER FORMATION, AND TRANSCRIPTIONAL ACTIVATION OF THE SERUM RESPONSE FACTOR. DER PROTEINS COUPLE RHO AND SRC TYROSINE KINASE DURING SIGNALING AND THE REGULATION OF ACTIN DYNAMICS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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B7FA9C745AE18CD9 CRC64;
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100.0%; Pred. No. 0.17;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98610 MW;
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853 AA;
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Matches 10; Conserv
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Run on:

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Sequence 3, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Patent No. 5200183
Sequence 2, Appli
Patent No. 5200183
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Appl
Sequence 5, Appli
Sequence 2, Appli
Sequence 66, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08899595
Patent No. 6111072
GENERAL INFORMATION:
APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Larcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY D.S.

ZIP: 20007-5109

ZIP: 20007-5109

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,595

FILING DATE: 24-JUL 1997

CLASSIFICATION NUMBER: US/08/899,595

PILING DATE: 26-AUG-1996

PILING DATE: 26-AUG-1996

PROM APPLICATION NUMBER: US/08/8996

PILING DATE: 25-AUG-1996

PILING DATE: 25-AUG-1997

ATPONENTYANDAN NUMBER: US/08/8996

PILING DATE: 25-AMR-1997

ATPONENTYANDAN NUMBER: DS-MAR-1997

ATPONENTYANDAN NUMBER: DS-MAR-1997

ANAME: ALCANDAN A BOATE

ANAME: ALCANDA
US-09-220-641-5

US-08-179-558-66

US-08-347-18B-1

US-08-445-050-7

US-08-445-050-7

US-08-204-691-3

US-08-204-691-7

US-08-347-718B-2

US-08-347-718B-2

US-08-347-718B-2

US-08-347-718B-2

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US-08-347-718B-2

US-08-345-050-2
                                                                                                                                                                                                                                                                                                                                   US-08-204-691-2
US-08-370-223-13
US-09-219-849-5
US-08-728-323A-2
US-07-609-716-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 049441/0112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29,768
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stephen A. Bent
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-595-3
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                             June 20, 2001, 12:06:45; Search time 14.07 Seconds (without alignments) 800.345 Million cell updates/sec
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Sequence 2, Appli
Sequence 2, Appli
Patent No. 5202236
Patent No. 5202236
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Sequence 10, A
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Sequence 4,
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1 MPLVKRNIDPRHLCHTALPR......AVEXSDSEDDSEFDEVDWLE
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 ARPQYYKLIEECISQIVLHKNGADPDFKCRHLQIEIEGLIDQMIDKTKVEKSEAKAAELE 528
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                                                                                                                                                                                                      360 LINALITPAEELDFRVHIRSELMRLGLHQVLQDLREIENEDMRVQLNVFDEQGEEDSYDL 419
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                                                                                                                        -- DRLSVSVTQLDPKEEELS-
    No. 1.3e-15;
smatches 183; Indels 193;
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                      Mismatches
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TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
STREFF
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FILING DATE:
CLASSIFICATION:
    Pred.
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Patent No. 5985574
GENERAL INFORMATION:
APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
Best Local Similarity 25.4%; Pr
Matches 148; Conservative 59;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPP----PPPPPLPSALSTSSLRASMT 345
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APPLICANT: Natumity, Shuh
APPLICANT: Tatahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                64; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 318.5; DB 2;
Pred. No. 1.7e-15;
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; Patent No. 6111072
NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: UNFITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
24.2%;
                                                                                                     (650) 343-4341
                                                                                                                                                                                                             1255 amino acids
                                                                                                                          TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-09-080-897-4
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 138; Conserva
                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                     linear
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51 IFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQ 110
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                                            -TNPSY --- FFDLWKEKMLQDTEDKRK - EKRKQKQKNLDRPHEPEK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 LFDRK-----YRDDGKEGLKFY- 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 318.5; DB 4;
; Pred. No. 1.7e-15;
64; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : SCIENCE & TECHNOLOGY LAW GROUP
75 DENISE DRIVE
                                                                                                       511 LRK-----VEEQREQE-----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Leon, Pedro E. TITLE OF INVENTION: Modulators of Actin
                                                                                                                                                  762 LRRPNWSKFVAEDLSQDCFWTKVKEDRFENN 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
                                                                                                                                                                                                                                                       Sequence 4, Application US/09323735 Patent No. 6197932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                       King, Mary-Claire
Lynch, Eric D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%;
24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Morrow, Jan E. APPLICANT: Welcsh, Piri I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 24.2 Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-09-323-735-4 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                    Lee, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
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                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 IFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 LINALITPAEELDFRVHI---RSELMRLGLHQVLQELREIENEDMKVQLCVFDEQ-GDED 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 LFDRK-----YRDDGKEGLKFY- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLDRPHEPEK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 VPRAPHDRRREWQKL------AQGPELAEDDANL------LHKHIEVANGPASH 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 TAR--HELQVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQKQDLEAFVSKLTGEVAK 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPP----PPPPPLPSALSTSSLRASMT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 STPPPP-----VPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 CIPPPPQLPGSAAIPPPPLPGVA----SIPPPP-PLPGATAI--PPPPPLPGATAIPPP 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 PVARAAPVCETVPVHPLPQGEVQGLPPPPPPP----LPPPGIRPSSPVTVTALAHPPSG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 177; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 FETRPQTYVDHMDGSYSLSALPFSQMSELLTRA----EERVLVRPHEPPPPPPMHGAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%; Score 318.5; DB 4; Length 1255; 24.2%; Pred. No. 1.7e-15; ive 64; Mismatches 192; Indels 177;
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                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    049441/0112
                                                                                                                                                                                                                                                                PILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-242701
FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 9-90170
FILING DATE: 25-MAR-1997
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-MAR-1997
ATTORNEY/ACENT INFORMATION:
NAME: Stephen A Rent
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.2%
Matches 138; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stephen A. Bent
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-899-595-1
                                          Washington
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                                                                                                   20007-5109
ADDRESSEE:
STREET: 30
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US-09-080-897-2
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                                                                                                                                                                                                                                                                                                                                                                                                                               455 LHPTPSTAPGPHVPLMPPSPPSQVIPASEP----KRHPSTLPVISDARSVLLEAIRKGIQ 510
424 LIEECVSQIVLHKNGTDPDFKCRHLQIDIERLVDQMIDKTKVEKSEAKATELEKKLDSEL 483
                                                                                                                                                                                                                                                                                                                                                   399 PVARAAPVCETVPVHPLPQGEVQGLPPPPPPPP----LPPPGIRPSSPVTVTALAHPPSG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LHKHIEVANGPASH
                                                                                                                                                                                                                   484 TAR--HELOVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQKQDLEAEVSKLTGEVAK
                                                                                                               235 FETRPOTYVDHMDGSYSLSALPFSQMSELLTRA----EERVLVRPHEPPPPPMHGAGD
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APPLICATION NUMBER: US/09/080,897
                                        ----AQGPELAEDDANL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lee, Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 LRK-----VEEQREQE-----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
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Patent No. 5985574
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King, Mary-Claire
Lynch, Eric D.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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STATE: CALIFORNIA
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APPLICANT:
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US-09-080-897-2
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                                                                                                                                                                                                                                                                                                                                                                                                     477 KKLDSELTAR--HELQVEMKKMESDFEQKLQDLQ------GEKDALHSE-KQQIATEK 525
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                                                                                                                                                                                       92 ---LQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYDVCEQPPPLNILTP---YRDDGK 145
                                                                                                                                                                                                                                                                            ----TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLD 185
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                                                                                                                                       308 LINALITPAEELDFRVHIRSELMRLGLHQVLQDLREIENEDMRVQLNVFDEQGEEDSYDL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 ALAHPPSGLHPTPSTAPGPHVPLMPP----SPPSQVIP-ASEPKRHPSTLPVISDARSVL 501
                                                                                          51 IFGELFNEAHSFSFRVNSLQERV------DRLSVSVTQLDPKEEELS--- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 MDGSYSLSALPFSQMSELLTRAEE-----RVLVRPHEP----PPPPPMHGAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPPPPSALSTSSLRASMTSTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PLP-GEA-GMPPPPPLPGGPGIPPPPFFGGP----
                                               Indels 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 LEAIRKGIQLRK-----VEEQREQE-----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :|||:
751 --LYKPEVQLRRPNWSKLVAEDLSQDCFWTKVKEDRFENN 788
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    DB 2;
Score 313.5; DB Pred. No. 4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SCIENCE & TECHNOLOGY LAW GROUP 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CADDRESSED ADDRESS:
CADDRESSED: SCIENCE & TECHNOLOGY LAW GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09323735
Patent No. 6197932
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lee, Ming
APPLICANT: MOREOW, Jan E.
  10.5%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MOLTOW, Jan E. APPLICANT: Welcsh, Piri L. APPLICANT: Leon, Pedro E.
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: HILLSBOROUGH
STATE: CALTECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 SAGIPPPPP-----
  Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                              146 EGLKFY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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296 CISSATGLIENRPQSPATGRTPVFVSPTPP---PPP---PPLPSALSTSSLRASMTSTP 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 PPVSTPPPTSSPPPVTASPPPVSTPPPS-----SPPPATPP---PASPPPATPP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 VCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPG- 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 CIAVA-GVLGQAPSNPPTS-TP--ATPTPPASTPPPTTQAPPTP------TATP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 261; DB 1; Length 214;
; Pred. No. 3.4e-12;
16; Mismatches 57; Indels
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APPLICANT: Barton, Kenneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
                         APPLICANT: Barton, Kenneth A TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT.INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-217-327-6; Sequence 6, Application US/08217327; Sequence 6, Application US/08217327; Patent No. 5474925; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Quarles and Brady STREET: P.O. Box 2113
                                                                                                                        ADDRESSEE: Quarles and Brady
STREET: P.O. Box 2113
CITY: Madison
                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 SPVOTPLTSPPAPPTEA-PA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 --PHVPL-MPPSPPSQVIPA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.8%
Best Local Similarity 35.5%
Matches 71; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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US-08-217-327-4
                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 AKPIPTCISSATGLIENRPQSPATGRIPVFVSPTPPPPPPPPPLPSALSTSSLRASMTSTPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 PP-----VPPPPP-PPATALQAP------AVPPPPAPLQIAPGVLHPAPPPIAPPL--393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---VQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPP----PPLPPPGIRPSSPVTVT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 LINALITPAEELDFRVHIRSELMRLGLHQVLQDLREIENEDMRVQLNVFDEQGEEDSYDL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYDVCEQPPPLNILTP---YRDDGK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526 ODLEAEVSOLT-GEVAKLTKELEDAKKEMASLSAAAITVPPSVPSRAPVPPAPPLPG--- 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 ALAHPPSGLHPTPSTAPGPHVPLMPP----SPPSQVIP-ASEPKRHPSTLPVISDARSVL 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DRLSVSVTQLDPKEEELS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 ARPQYYKLIEECISQIVLHKNGADPDFKCRHLQIEIEGLIDQMIDKTKVEKSEAKAAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAGIPPPPP-------PLP-GEA-GMPPPPPPPPPPPPPPPPPPPPPPPPGGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 LEAIRKGIQLRK-----VEEQREQE-----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LYKPEVQLRRPNWSKLVAEDLSQDCFWTKVKEDRFENN 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 177;
                                                                                                                                         FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/080,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/08217327
; Patent No. 5474925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 IFGELFNEAHSFSFRVNSLQERV-
                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-323-735-2
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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US-08-217-327-4
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273 VRPHE-PPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPL 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 PPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPP--PPPPPLPPPGIRPSSPVTV-TA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Koichi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
APPLICANT: Randy, Allen
ITILE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
NUMBER OF SEQUENCES: 10
                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,545B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 PYKPPVPTPPVKPPTTPAP--PYKPPSPP---LPPVRTKK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 246.5; DB :
Pred. No. 5.9e-11
8; Mismatches 9
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/068001
TELECOMMUTCATION INFORMATION:
TELECHONE: 202/783-5070
TELEPHONE: 202/783-5331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSBE: Fish & Richardson P.C. STREET: 601 Thirteenth Street, NW CITY: Washington
                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/09262653A
; Patent No. 6166294
                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%;
                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                           : 297 amino acids amino acid
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Best Local Similarity 34.5:
Matches 76; Conservative
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-580-5458-6
                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 HEPP-----PPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPV--FVSPTPP- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 HSPPPPYHYESPPPKH----SPPPPTPVYK-----ҮКSPPPPMHSPPPPYHFESPPPK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PPPP------PLPSALSTSSLRASMTSTPPPPV------PPPP-------356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 --PPPATALQAP-----AVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 ---APVHHYKYKSPPPPTPVYKSPPPPEHSPPPPTPVYKYKSPPPPHHYKYKSPPPPTPVYKYK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 306;
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APPLICANT: Koichi, Fulisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
APPLICANT: Randy, Allen
TITLE OF INVENTION: COTTON FIBER TISSUE-SPECIFIC GENES
                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.7%; Score 259.5; DB 1
Best Local Similarity 30.6%; Pred. No. 6.8e-12;
Matches 83; Conservative 12; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 HPPSGLH--PTPSTAPGP---HVPLMPPSPP 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 SPPPРМНSPPPVYSPPPРКННҮSYTSPPPP 303
                                                                                                                                                                                                                                                                                                                                         NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERNCE/DOCKET UNMBER: 1122990831
TELECOMMUNICATION: 1000831
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C. STREET: 601 Thirteenth Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08580545B Patent No. 5932713 GENERAL INFORMATION:
                                                                                                      COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6:
                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             608-251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-217-327-6
                                                           COMPUTER READABLE FORM:
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ADDRESSEE: F1sh & Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                  FILING DATE:
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STATE:
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480 HHHHQQQQQQQQQQQQQHHGN----SGPPP----PGAFPHPLEGGSSHHAHPY 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 -TVGPGPLPPAGPSGLPSLPPPPAAPASG----PPLSATQIKQEPAEEYETPES---PVP 737
                                                                                                                                                                                                                                                                                              198 HDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQTYVDHMDGSYSLSALPF 257
                                                                                                                                                                                                                                                                                                                                                                                   258 SOMSELLTRAEERVLVRPHEP-----PPPPPMHGAGDAKPIPTCISSATGLIENRPQSPA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 TGRTPVFVSPTP-----PPPPPPPLP----SALSTSSLRASMTSTP---PPPVPPPPPP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 YGKRAPSPGAYKTATPPGYKPGSPPSFRTGTPPGYRGTSPPAGPGTFKPGSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETVPVHPLPQGEVQGLPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPFGPHV
                                                                                                                                                                                                                                               Mismatches 149; Indels 105;
                                                                                                                                                                                                    Length 1185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 IRKGIQLRKVEE-----QREQEAKHER----IENDVATILSRRIAVE 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRALTOR:
APPLICANT: FERRALTOR:
APPLICANT: FERRALTOR:
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARR: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                  Score 246.5; DB 4
Pred. No. 3.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A55556-3/BIR TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-642-255-32
; Sequence 32, Application US/08642255
; Patent No. 5773249
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IBM PC compatible
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....r.rERISTICS:
....r. 1185 amino acids
TYPE: amino acid
TOPOLOGY: 11**
                                                                                                                                                                                                    Query Match 8.3%;
Best Local Similarity 25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                 Matches 103; Conservative
  INFORMATION FOR SEQ ID NO:
                                                                                                          ; MOLECULE TYPE: protein US-09-041-886-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 РРА-----РАРРТКАРТРРУКРРАРДРАРДТКАРТРРУКРРАРДРИТКАР-----ТРРFК 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 PPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPP--PPPPPLPPPGIRPSSPVTV-TA 447
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APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 LAHPPSGLHPT-PSTAPGPHVPLMPPSPPSQVIPASEPKR 486
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 246.5; DB Pred. No. 5.9e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                           ATTORNEY/AGENT INFORMATION:
NAME: Eretschneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/068001
TELECOMMUNICATION:
TELECHONE: 202/783-5070
TELEPHONE: 202/783-5331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET UNBER: P-LJ 2626
TELECOMMUNICATION:
TELEPHONE: (619) 535-9001
US/09/262,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/041,886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                               TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         TYPE: amino acids
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.3%;
Best Local Similarity 34.5%;
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-262-653A-6
APPLICATION NUMBER:
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                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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; MOLECULE TYPE: protein US-07-609-716-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                            Score 244; DB 1; Length 330;
Pred. No. 1e-10;
5; Mismatches 92; Indels
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Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65, Application US/07609716

Sequence 65, Application US/07609716

GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 PGPPGPPGPPGPPGAPGPPGPPGPPGPAGPVGSP 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
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Pour Embarcadero Center,
San Francisco
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FILING DATE: 06-NOV-1990
TELEPAN: (415) 494-8701
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
      (415) 494-8700
                                                                                                                                                                                                                                                          Query Match 8.2%;
Best Local Similarity 34.1%;
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-642-255-32
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MEDIUM TYPE: Floppy
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TOPOLOGY: 11n
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94111
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US-07-609-716-65
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                                                                                                                275 PHEPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPAA 334
                                                                                                                                                                                                                                                                                                                                                                     51 PGPPGPPGPPGPAGPV------GSPGAP------GPPGPPGPPGP 89
                                                         46;
  Length 408;
                                                         Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/08475411A
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
Query Match 8.2%; Score 244; DB 1;
Best Local Similarity 34.1%; Pred. No. 1.3e-10;
Matches 74; Conservative 5; Mismatches 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 PGPPGPPGPPGAPGPPGPPGPPGPPGPVGSP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 AHPPSGLHPT-PSTAPGPHVPLMPPSPPSQVIPASEP 484
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REFERENCE/DOCKET NUMBER: A-55186-9/RFT/MTK
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/475,411A
FILING DATE: 07-JUN-1995
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TELEPHONE: 415-781-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                     393 LVQPSPPVARAAPV----CETVPVHPLPQGEVQGLPPPPPPPPPPPPPGIRPSSPVTVTAL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 408;
                                                                                                                                                                                                          Indels
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STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-478-029A-65.
Sequence 65, Application US/08478029A
Patent No. 6184348
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Fructional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER.OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,029A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFISTRATION NUMBER: 31,801
REFISCOMMUNICATION INFORMATION:
                                                                                                                                                          Score 244; DB 4;
Pred. No. 1.3e-10;
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                                                                                                                                                          Query Match 8.2%;
Best Local Similarity 34.1%;
Matches 74; Conservative
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MEDIUM TYPE: Floppy disk
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-411A-65
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STATE: CA
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Pred. No. 1.3e-10;
5; Mismatches 92; Indels
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Best Local Similarity 34.1%;
Matches 74; Conservative
                                           408 amino acids
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 408 amino acid
                                                                                   single
                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                             TYPE: amino acid
STRANDEDNESS: sir
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Search completed: June 20, 2001, 12:07:08 Job time: 23 sec

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extensin class 1
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proline-rich prote
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Copyright (c) 1993 - 2000 Compugen Ltd.
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2981
1 MPLVKRNIDPRHLCHTALPR.
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Perfect score:
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Run on:

ALIGNMENTS

Sequence:	1 MPLVKRNIDPRHLCHTALPRAVEYSDSEDDSEFDEVDWLE 559	14.
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5	4 4 5 5
Searched:	219241 seqs, 76174552 residues	
Total number of !	Total number of hits satisfying chosen parameters: 219241	
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_68:*
1: pir1:*
2: pir2:*
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4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	hypothetical prote	extensin homolog T	unknown protein [i	extensin - Volvox	hypothetical prote	hypothetical prote	E	wiskott-aldrich sy	Wiskott-Aldrich sy	\sim		diaphanous protein	extensin homolog F	hypothetical prote	₽	probable Pto kinas	hypothetical prote	o	atrophin-1 related	hypothetical prote	extensin-like prot	hypothetical prote	ise (EC	pistil extensin-li	formin isoform IV	probable cell wall	pistil extensin-li	hypothetical prote	•
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Score	598	363	362.5	348.5	346.5	334	332.5	326.5	323.5	323.5	320	318.5	316	310	309	308.5	305.5	305.5	304	292.5	291.5	290.5	287.5	286.5	286.5	286	285.5	285.5	285.5
Result No.	.	7	e	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	26	27	28	29

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Cross-references: EMBL: Z81106; PIDN: CAB03220.1; GSPDB: GN00019; CESP: R06C1
0019; CESP:R06

m.

18;

Length 507;

DB 2;

20.1%; Score 598;

Query Match

Best Local Similarity 28.8%; Pred. No. 8.4e-25; Matches 170; Conservative 88; Mismatches 214; Indels 118; Gaps	MPLVKRNIDPRHLCHTALPRGI-KNELECYTNISLANIIRQLSSLSKYAEDIFGELFNEA 59	MPLTKRAVSPVNLSRGTIPSTIHRDELQCTANGTIANLVRQLSSLSKHAENIFGEIYHDA 60	60 HSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQLFDRKTLPI 119	DRLHKKVEDLDSNSDQATLNEANMRKAFKSSMLVDQHILDRSTLPT 120	LNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKRKEKRKO 179	121 ALTEIXAKCDPPPDLDALNPYRDSEIPALSLYTNPSFFFDLWKKFTLKEVAERPR 175	180 KQKNLDRPHEPEKVPRAPHDRRREWQKLAGGPELAEDDANLLHKHIEVANGPASHFETRP 239	RVKSPNDGSKSPKKRRKQPGQGP	240 OTYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPPPPPPPMHGAGDAKPIPTCISS 299	GSRINQONEVESFPEEYQAPQ 236	300 ATGLIEN-RPQSPATGRTPVFVSPTPPPPPPPPBALSTSSLRASMTSTPPPPVPPP 355	ALGLOLNEKNOHPSNMVAPIGMIMHHHPQQNVHPSQQRGGAPAAARGSPNVKRPTEAPPP 296	356PPPPATALQAPAVPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARA 403	SIDDDDDDLPPPPPPLLMNTSIVHQLPAEAPSTIQFVEPSAAPPTN 356
al Similarity 28.8%, 170; Conservative	MPLVKRNIDPRHLCHTALPRG	MPLTKRAVSPVNLSRGTIPST	HSFSFRVNSLQERVDRLSVSV	HIINHKSNTLQQRIDRLHKKV	PLOETYDVCEOPPPLNILTPY	ALTEIYAKCDPPPDLDALNPYF	KOKNLDRPHEPEKVPRAPHDRI	RVKSPNDGSKSPKKRI	OTYVDHMDGSYSLSALPFSQM9	TAYNDMQHRNRQISGSRINQQNEVFSFPEE-	ATGLIEN-RPOSPATGRTPVF	ALGLQLNFKNQHPSNMVAPIGN	PPPPATALQAP	VNLDHLPPPDMSILSIDDDDDI
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Matches 122; Conserv
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                                                                                                                                                                                                                                                                                              cyteria homolog T9EB.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999
C;Accession: T06291
R;Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel submitted to the Protein Sequence Database, April 1999
A;Reference number: 215588
A;Reference number: 215588
A;Residues: 1-760 cBEV>
A;Residues: 1-760 cBEV>
A;Residues: 1-760 cBEV>
A;Experimental source: cultivar Columbia; BAC clone T9E8
A;Map position: 4
A;Note: T9E8.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNKNOWN protein [imported] - Arabidopsis thaliana
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiAccession: G86441

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Pitle: Sequence and analysis of chromosome I of the plant Arabidopsis.
                                   LKICNFCPFLCFPHCCPLSASFFNSRSLSDPSTTSTTSNGYKLGCSVICSSGSKGKGAG 416
                                                                                                           ---DARSDLLAQIQSGIK 455
  -LAHP 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 LVRPHEPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 PSALSTSSLRASMTSTPPPPPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 PLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPPGIRPSSPVTVTALAHP 451
                                                                             452 PSGLHPT-PSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVLLEAIRKGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPHSSPPPHSPPPHSPPPIYPYLSPPPPT---PVSSP---PVYS 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 PSGLHPTPSTAPGPHVP-----LMPPSPPSQVIPASEPKRHPSTLPVIS 495
                                                                                                                                                                                LRKVEEQREQEAKHERIE-NDVATILSRRI--AVEYSDSEDDSEFDEVDW 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 760;
404 APVCETVPV----HPLPQG----EVQGLPPPPPPPPPPPGIRPSSPVTVTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.2%; Score 363; DB 2; 36.4%; Pred. No. 3.5e-12; ive 13; Mismatches 82.
                                                                                                         84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: G86441
A, Status: preliminary
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Best Local
                                                                                                                                                             511
                                                                                                                                                                                                 456
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                                     357
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biogenesis in Volvox
                                                                                                                                                                                                                                                         18;
A;Molecule type: DNA
A;Residues: 1-1201 <STO>
A;Cross-references: GB:AE005172; NID:g11136725; PIDN:AAG31306.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Volvox carteri
C;Date: 04-Dec:1992 #sequence_revision 04-Dec-1992 #text_change 21-Jul-2000
C;Accession: S2267; S21006
C;Riccession: H; Hallmann, A:; Wenzl, S.; Sumper, M.
EMBO J. 11, 2055-2062, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EERVLVRPHE-----PPPPPMHGAGDAKP 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 IPTCISSATGLIENRPQSPATGRTPVFVSPT-----PPPPPPPPPPLPSALSTSSLRASMTS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489 PPPLFTSTTSFSPSQPPPPPPPPPPPTTSFSPSQ-P 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 -LHKHIEVANGPASHFETRPQTYVDHMDGSYSLSA-----LPFSQ------MSELLTRA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 -RPPPPPPPPSSRSIPSPSAPPPPPPPPSFGSTGNKRQAQPPPPPPPPPPPTRIPAAKC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PPPGIRPSSPVTVTALAHPPSGLHPTP----STAPGPHVPLMPPSPPSQVIPASE 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPPPPPTSHSGSIRVGPPSTPPPPPPPRANISNAPKPPAP--PPLPPSSTRLGAP 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 LLTRAEERVLVRPHEPP-----PPPPPMHGAGDAKPI-----PTCISSATGLIENRPQS 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 PATG-RTPVFVSPTPPP----PPPPLPSALSTSSLRASMTSTPPPPVPP-----PPPPPA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 PKTSPPPPRVPSSPPPPPRVASPSPPPPRVSSPSPPPPRS 327
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                              |:|||
| S22 PQKVPTPIVNGDETGGLPIEAFSRVQELFSGVDLAENGDDAALWLLKQLAAINDAKEFTR 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 FRHKGSFYFNSPDSEEETNTSSAADSSDEGFEAIQRPRIHIPFDNDDTDDITLSVAHESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 TPPPPVP------PPPPPPATALQAPAVPPPAPLQIAPGVLHPAPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389 IAPPLVQPSPPVARAAPVCETVPVHPLP-----QGEVQGLPPPPPPPPPL-----
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                                                                                                                                                                                                                                                         153;
                                                                                                                                                                                              Length 1201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Reference number: $22697; MUID:92289669 A)Accession.
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                 190 PEKVPR-----APHDRRREWQKLAQGPELAE--DDANL----
                                                                                                                                                                                              12.2%; Score 362.5; DB 2; 28.5%; Pred. No. 6.1e-12;
                                                                                                                                                                                                                                                         24; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 348.5; DB 2; 37.0%; Pred. No. 1.2e-11; Live 19; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extensin - Volvox carteri (fragment)
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P 414 Db 632 PPPPVHSPPPPVYSPPPPVKSPPPPVKSPPPPVYSPPLLPPKMSSPPTQTPVNS Ov 483 EPKRHPS 489	474 Db 688 PPPRTPS	φ. Ο	ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A, Authors: Hunter, J.L.; Jenkins, J. C.A.: Li, J.H.: Li, Y.: Lin, X.: Lin	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, J. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.		A; Molecule type: DNA A; Residues: 1-907 <sto> A; Cross-references: GB:AE005173; NID:g6751696; PIDN:AAF27679.1; GSPDB:GN00141 C; Genetics: A; Gene: T7P1.21 A; Map position: 1</sto>		Gaps 26; Qy 70 QERVDRLSVSVTQLDPKEBELSLQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYDVCE LS 77 Db 222 KERFDMMEIDEEEEKKESTSPQTGKTSSSRVLSPSESFSDSKSSFGSRNSFCG	E 294 QY 130 QPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQDTEDKKKEKRKGKQK	T 328 Qy 183 NLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGP 181		439			P 576 Qy 434 -PPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLP 432
TALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHP SPSPPPPSPPPSPPPRSSPSSPSPPPPWSSPPPPPPRSSPS	LPQGEVQGLPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSP	376 - PPPPASSPPPPPREPPESPPPSPPPPPATAAANPPSPA-PSRSRAGGPPLGTRPPPP 475 PSQ 477 1 1- 431 PPE 433	hypothetical protein At2g15880 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Preb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84534	Rillo, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, with a state of the control of	Nature 402, /ol./ps, 1987, 1987 Additional Arguntana A	A;Status; pratiminary A;Molecule type: Index A;Molecule type: I-727 cSTO> A;Cross-references: GB:AE002093; NID:g5306245; PIDN:AAD41978.1; GSPDB:GN001 C;Genetics: A2g15880 A;Gene: At2g15880	11.6%; Score 346.5; DB 2; Length 727; Larity 25.8%; Pred. No. 2.5e-11;	des 141; Conservative 54; Mismatches 183; Indels 169; Gaps 18 LPRGIKNELECVINISLANIRQLESKYAEDIFGELFNEAHSFSFRVNSLQERVDRLS 77 11	242 IPRSIGNMKNLNEIIFKDNSLGGCFPSEIGKLAN-VNVFDASMNSFTGVLPPSF 294 78 VSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYDVCEQPPPINIL 137	VGLTSMEEFDISGNKLTGFTPIPENICKLPKLVNLT TPYRDDGKEGLKFYINPSYFFDLWKEKMLQDTEDKRKEKRKQKQ	329 YAYNYENGGGDSCVPGSQKQIALDDTRNCLPDREKQRSAKECAVVISRPVDCSK 182KNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANL : : : :	DKCAGGSSQATPSKSPSPVPTRPVHKPQPPKESPQPNDFYNQSPVKFRRSPPPQQP LHKHLEVANGPASHFETRPQTYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEP 	-HHHVVHSPPPASSPPTSPPVHSTPSPVHKPQPPKESPQPNDPYDPPPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPP	OSPVKERRSPPPPPVHSPPPPSPI*HSPPPPPVY-SPPPPPVY -PPPLPSALSTSSLRASMTSTPPPPVPPPPTALQAPAVPPPPAPLQIAPGV	SPPPPPPVXSPPPPPPVHSPPPVHSPPPVHSPPPPVHSPPPPVHSPPPP

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A; Molecule type: DNA
A; Residues: 1.574 <CON>
A; Cross-references: EMBL:298980; NID:e1060691; PIDN:CAB11718.1; GSPDB:GN00066; SPDB:S
A; Experimental source: strain 972h-; cosmid c4F10
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dmod
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R;Zankel, T.C.; Ow, D.W.
Subnitted to the EMBL Data Library, December 1997
A;Description: A Wiskott-Aldrich Syndrome protein homolog in Schizosaccharomyces
A;Reference number: 222575
                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                             172 KRKEKRKQKQKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAED-DANLLHKHIEVANG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                        144 KGSSRHAPNNSNIQPPSAAPPVP-GKENYNAVGSKSPNEPELLNSLDPSLIDSLMKMGIS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 PASHFETRP--QTYVDHMDGSYSLSALPFSQMSELLTRAEERV--LVRPHEPPPPPMHG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 AGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSP----TPPPPPPPPPPSALSTSSLRA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PPPPPPATALQAPAVP-----PPPAPL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIAPGVLHPAPPPIA-----PPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPP 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSLPPSAPPSLPPSAPPSLPMGAPAAPP--LPPSAPIAPPLPAGMPAAPPLPPAAPAPP 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEPKRHPSTLPVIS-----DARSVLLEAIRKG----IQLRKVEEQRE----- 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPPLP---PPGIRPSSP--VIVIALAHPPSGLHPTPSTAP--GPHVPLMPPSPPSQVIPA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDQIAENADFVKAYLNESAGTPTSTSAPPIPPSIPSSRPPERVPSLSAPAPPPIPPP---
                                                                                                                                                                                                                                                                                                                                               Indels 103;
                                                                                                                                                                                                                                                                                                 Length 574;
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                                                                                                                                                                                                                                                                                                 Query Match 11.0%; Score 326.5; DB 2; Best Local Similarity 26.6%; Pred. No. 2.1e-10; Matches 122; Conservative 57; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QEAKHERIENDVATILSRR---IAVEYSDSEDDSEFD 553
                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Experimental source: strain JS21
                                                                                                                                                                                A;Gene: wspl; SPDB:SPAC4F10.15c
A;Map position: 1
A;Introns: 72/3; 519/3; 564/1
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A; Introns: 72/3; 519/3; 564/1
A; Reference number: 221813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-574 <ZAN>A; Cross-references: EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T43556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                  actin-depolymerizing protein N-WASP, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: 37-Apr-1998 #sequence_revision 01-May-1998 #text_change 05-Nov-1999
C;Accession: 572273
R;Miki, H.; Miura, K.; Taknawa, T.
EMBO J. 15, 5326-5335, 1996
A;Title: N-WASP, a novel actin-depolymerizing protein, regulates the cortical cytoskelet A;Teference number: 872273; MUID:97050838
A;Accession: 872273
A;Accession: 572273
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-505 AMIX
A;Residues: 1-505 AMIX
A;Esciences: EMBL:D67066; NID:91644231; PIDN:BAA11082.1; PID:d1011742; PID:g16442
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #15Kott-aldrich syndrome protein homolog 1 - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38819 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 R;Connor, R:, Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |: || : || : |: || || || EAKKFRKAVTDLLGRRQRKSEKRRDPPNGPNLPMATVDIKNPEITTNRFYGPQINNISHT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRREWOKLAQGPELAEDD----ANLLHKHIEVANGPASHFETRPQTYVD-----HMDGS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSLSALPFSQMSELLTRAEERVL-------VRPHEPPPPPPMHGAGDAKPI 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :: | |: | : | : | : | KEKKKGR-AKKRRTFADIGTPSNFQH-----IGHVGWDPNTGFDLNNLDPELKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDMCGISEAQLKD---RETSKVIYDFIEKTGGVEAVKNELRRQAPPPPPFSRGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVPVHPLPQGEVQG-LPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.2%; Score 332.5; DB 2; Length 5 Best Local Similarity 23.5%; Pred. No. 8.9e-11; Matches 135; Conservative 66; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 KRKEKRK------OKOKNLDRPHEPEKVPRAP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQPPPLN-----GLTPYRDD-----GKE-----GLKFYT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NP--SYF---FD-----LWKEKMLQD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 PTSGIVGALMEVMQKRSKAIHSSDEDEDDEDF 497
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TSSLRA 342 34ALAA 306 PPPAPL 375 111 1 PPPPP 428 11PPVPT 419 SQVIPA 481 3 SQVIPA 481 3 SQVIPA 481 5 SQVIPA 536 KTSNPP 536 ke domains	TSSLRA 342 11 1 1 1 1 1 1 1 1 1
PPPAPL 375	PPPAPL 375 PPPPAPL 375 PPPPP 428
LPPPPP 428	LPPPPP 428
SQVIPA 481 519 KTSNPP 536 KTSNPP 536 29-Oct-199	SQVIPA 481 519 KTSNPP 536 KTSNPP 536 29-Oct-1999 TD:9600118 R8; 27; Gaps TTDKRK 174PPA 797 VANGPA 232 VANGPA 232 VSPPP 844 PPMHGA 287 I SPREEEK 897
KTSNPP 536 29-Oct-199	xTSNPP 536 XTSNPP 536 29-Oct-1999 TD:9600118 88; TD:9600118 RB; VANGPA 174 PPA 797 VANGPA 232 :: VANGPA 232 :: PPMHGA 287
29-Oct-199 ke domains	29-Oct-1999 ke domains. TD:9600118 88; 27; Gaps TEDKRK 174PPA 797 VANGPA 232 : VASPPP 844 PPMHGA 287
29-Oct-199 ke domains	29-Oct-1999 ke domains. TD:9600118 88; 27; Gaps TEDKRK 174PPA 797PPA 797 VANGPA 232 :: VASPPP 844 PPMHGA 287
ke domain	Ke domains. 1D.9600118 88; 77; Gaps 7FEDKRK 174 PPA 797 VANGPA 232 :: VSSPPP 844 PPMHGA 287
	aps 174 797 232 844 897
Fred. No. 76-10; 10; Mismatches 158; Indels 127; Gaps	
aps 174 797	
aps 174 797 232 844	

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Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, nsen, N.F.; Hughes, B.; Huizar, L.
ature 408, 816-820, 2000
2000
316-820, 2000
317-34thors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, E.; Kim, A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia, Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Print, Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Accession: G86292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AE005172; NID:98927662; PIDN:AAF82153.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pothetical protein AAF82153.1 [imported] - Arabidopsis thaliana
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                              -----NGEA--FSTRCDVFFRCIFGTCGQWNFPIDPCPQNPFLPPPATLPPPL 346
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328 -----PPPLPSALSTSSLRASMTSTP---PPPVP--PPPPPATALQAPAV--PPPPAP 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 PPPPPPPPPSALSTSSLRASMTSTPPPPVPPPPPP---ATALQAPAVPPPPAP---LQI
                                                                                                                          375 LQIAPGVLHPAPPPI----APPLVQPSPPVARAPVCETVP--VHPLPQGEVQGLPP--
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Best Local Similarity 28.1%,
Matches 120; Conservative
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Molecule type: DNA
Residues: 1-1006 <STO>
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Ritheologis, A.: Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudfacs, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719
                                                                         J.; Mewe
                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                    R.; Argiriou, A.; De Simone, V.; Hoheisel,
Database, July 1998
  Species: Arabidopsis thaliana (mouse-ear cress)
Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::|: | :|: | :| :| :| 342 HNICQLPNLVNLTYSYNYFSGQGGSCVPGGSR-----KEIALDDTRNCLASRPEQRSAQE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VHKPTPVPTŤPVQKPSPVPTTPVQKPS---PVPTTPVHEPSPVLATPVDKPSPVPSRP 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVLLEAIRKGIQL
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 138;
                                                                                                                                                                                                                                                                                                                                                                               Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYSPPPVHSPPP----PVHSPPPAPAHSPPPAPAPAPAPAPAYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 CAVVINRPVDCSKDKCAGGSSTPSKPSPVHKPTPVPTTP-----
                                                                                                                                                                                                                                        A; Experimental source: cultivar Columbia; BAC clone F1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPVFSPPPSQSP-PVVYSPPRPPKINSP---PVQSPPPAPV--
                                                                                                                                                                                                                                                                                                                                                                               10.6%; Score 316; DB 2; I 25.6%; Pred. No. 9.6e-10; tive 40; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKVEEQREQEAKHERIENDVATILSRRIAVEYS 544
                                            C,Accession: T05225
R,Bevan, M.; Vitale, D.; Liguori,
submitted to the Protein Sequence
                                                                                                                                                                                  A; Residues: 1-699 <BEV>
A; Cross-references: EMBL:AL031032
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                   A; Reference number: 215404
A; Accession: T05225
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KNLDRP--
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                                                                                                                                                                                                                                                                                    A; Map position: 4
A; Note: F1715.160
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                 C; Genetics:
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                                                                                                                                                                                                      diaphanous protein homolog pl40mbia - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 22-Oct-1999 #sequence_revision 22-Oct-1999
C;Accession: T31065
R;Watanabe, N.; Madaule, P.; Reld, T.; Ishizaki, T.; Watanabe, G.; Kakizuka, A.; Saito, EMBO J. 16, 3044-3056, 1997
A;Title: Pl40mbla, a mammalian homolog of Drosophila diaphanous, is a target protein for A;Reference number: 220961; MUID:97357293
A;Accession: T31065
A;Accession: T31065
A;Accession: T31065
A;Accession: T31065
A;Molecule type: mRNA
A;Residues: 1-1255 < MAT>
A;Residues: 1-1255 < MAT>
A;Residues: 1-1255 < MAT>
A;Rosidues: EMBL:U96963; NID:92114472; PID:92114473; PIDN:AAC53280.1
A;Note: binds to GTP-bound form of Rho and binds to profilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 IFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLDRPHEPEK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPP----PPPPPLPSALSTSSLRASMT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 STPPPP-----VPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSP 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 PVARAAPVCETVPVHPLPQGEVQGLPPPPPPPP----LPPPGIRPSSPVTVTALAHPPSG 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : | :| :| :| | : | 484 TAR--HELQVEMKKMENDFEQKLQDLQGEKDALDSEKQQITAQKQDLEAEVSKLTGEVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 LSKELEDAKNEMASLSAVVVAPSVSSSAAVPPAPPLPGDSGTVIPP--PPPPPLPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 LFPVLPPPSVTPSPVLPLP----PPSAPLPPPLSSSLPSPPLPLVLSPPPP---LPGGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 LFDRK----YRDDGKEGLKFY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.7%; Score 318.5; DB 2; Length 1255; Best Local Similarity 24.2%; Pred. No. 1.4e-09; Matches 138; Conservative 64; Mismatches 192; Indels 177;
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extensin homolog F1715.160 - Arabidopsis thaliana
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                                              485 KRHPSTL 491
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cell wall hydroxyproline-rich glycoprotein gene
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A;Residues: 1-744 <STO>
A;Cross-references: GB:AE005172; NID:g3157926; PIDN:AAC17609.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jul-2000
C;Accession: S06733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 IAPGVLHPAPPPI-----APPLVQPSPPVARAAP---VCETVPVH--PLPQGEVQGLPPP 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                614 -----PPSPLYYPDVTPSPPPPSPVYYPDVTPSPPPSPVYYPPVTPSPPPSPVYYP 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 SYSLSALPFSQMSELLTRAEERVLVRPHEPPP-----PPPMHGAGDAKPIPTCISS--AT 301
                                                                                                                                                                                                                                              302 GLIENRPQSPATGRTP----VFVSPTPPPPPPPLPSALSTSS----LRASMISTPPPPVP 353
                                                                                                                                                                                                                                                                                                                                                                                  ---PP----PPPPATALQAPAV--PPPPAPLQIAPGVLHPAPP-PIAPPLVQPSPPVARA 403
                                                                                                                                                                                                                                                                                                                                                                                                                           613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            667 SETQSPPPPTEYYYSPSQSPPPTKACKEGHPPQATPSYEPPPEYSYSSSPPPSFSYFP 726
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                                                                                                                                                                             Gaps
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A; Residues: 1-620 <KEL>
A; Cross-treferences: EMBL:X13885; NID:g19866; PIDN:CAA32090.1; PID:g19867
C; Superfamily: hydroxyproline-rich glycoprotein
C; Keywords: glycoprotein
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                                                                                                                                    Length 744;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 PPPPPMHGAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPT----
                                                                                                                               10.4%; Score 310; DB 2; Le 31.7%; Pred. No. 2.1e-09; ive 26; Mismatches 113;
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Genes Dev. 3, 1639-1646, 1989
A;Title: Specific expression of a novel ce
A;Reference number: S06733; MUID:90128263
A;Accession: S06733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 APVCETVPVHPLPQGEVQGLPPPP
                                                                                                                             Query Match
Best Local Similarity 31.78
Matches 97; Conservative
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Search completed: June 20, 2001, 12:09:05 Job time: 139 sec

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Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Collagen-like poly Collagen like prot

CLP protein sequen

Human atrophin I p Human ORFX ORF2085

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Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
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B43375
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Y21928
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     Human Neural-Wisko
Rat Neural-Wiskott
N-Wiskott-Aldrich
Human mDia Rho tar
Mouse Rho target p
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Mycobacterium tube
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **Controlly of the control of the co
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               - protein search, using sw model
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W37151
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W37151 standard; Protein; 783 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                    112 FORKTLPIPLQETYDVCEQPPPLNILTPYRDDGKEGLKFYTNPSYFFDLWKEKMLQD-TE 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atrfats1gsafhpv1phyatvprplnknsrpsspvnt-pssgppaakscawptsnfspl 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 ppsppimissppgkatgprpvlpvcvssp---vpqmppsptapngsldsvtypvspppts 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PPPPPPPLPSALSTSSLRASMTSTPPPPPPPPPPPPATALQ----APAVPPPPPPLQ 376
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                                                                                                                                                                                                                                                                                                                                                                                                    3 LVKRNI-DPRHLCHTALPRGIKNELECVTNISLANIIRQLSSL---SKYAEDIFG----- 53
                                                                    CDNA library. Two other isoforms, neural Mena+ (see W37151) and neural Mena++ (see W37153), are also disclosed. Unlike mammalian Ena (Mena, see W37148), neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and Evl genes (see also W2956-98) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is
                                                              Its amino acid
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                                                                                                                                                                                                                                                                                                                                                                      Indels 228;
                                                                                                                                                                                                                                                                                                                                         Length 787;
                                                            This protein comprises novel murine neural Mena++.
                                                                                                                                                                                                                                                                                                                                      12.1%; Score 360; DB 19; 23.1%; Pred. No. 4.2e-16; ive 81; Mismatches 196;
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                              Example 4; Page 60-63; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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W37151
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-ELFNEAHSFSFRVNSLQERVDRLSVSVTQL-----DPKEEELSLQDITMRKAFRSSTI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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vvgrkiqdhqvvincaipkglk------ynqatqtfhqwrdarqvyglnfgsked 96
                                                                                                                                                                                                            Neural Mena+ protein; mammalian Ena; Enabled protein; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This protein comprises novel murine neural Mena+. Its amino acid sequence was deduced from a cDNA clone (see V02998) obtained from a mouse brain cDNA library. Neural Mena+ contains an exon that introduces 244 amino acids between amino acids 238 and 239 of mammalian Ena (Mena, see W37148). Two other isoforms, neural Mena++ (see W3152), are also disclosed. Unlike Mena, neural Mena+++ (see W37153), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural tissue specific distribution. Based on the disclosed Mena and Evl genes (see also V02996-97) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. method of detecting a modulator of Mena activity/expression is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LVKRNI-DPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFG-----
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Best Local Similarity 23.0%; Pred. No. 6.6e-16;
Matches 152; Conservative 78; Mismatches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG (HUTC-) HUTCHINSON CANCER RES CENT FRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 58-60; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soriano P,
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                          Mouse neural Mena+ protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-101197/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of modulators of Mena and Ena-VASP-like genes and proteins
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                                  QD-TEDKRKEKRKQKQKNLDRPHEP--EKVPRAPHDRRR---
                                                                    --KHIEVANGPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell growth; cell motility; mouse
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                                                                                                                                                                                                                                                                                                                                                                       W37153 standard; Protein; 802
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This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a CDNA clone obtained from a mouse brain sequence was deduced from a cDNA clone obtained from a mouse brain comparing two other isoforms, neural Mena+ (see W37151) and neural Mena+ (see W37151), are also disclosed. Unlike mammalian can (Mena, see W37148), neural Mena isoforms exhibit neural cissue-specific distribution. Based on the disclosed Mena and Evl genes (see also V0296-98) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, cisolating and characterising endogenous and exogenous factors, cisolating and characterising endogenous and exogenous factors, cytoskeletal dynamic events involved in normal and abnormal cell corposed method of detecting a modulator of Mena activity/expression is
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used in control of cytoskeletal dynamic events in norm normal cell morphology, adhesion, motility, growth and
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Pred. No. 7.3e-16;
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                                                                                                                                                                                                                              Example 4; Page 63-65; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.0%;
22.5%;
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The present sequence represents a rat Neural-Wiskott-Aldrich syndrome protein (N-WASP). Wiskott-Aldrich syndrome (WAS) is a syndrome associated with recurrent infections and eczema, in which an afflicted patient hiss a tendency to haemmorhage. The protein and related cDNA sequences are used to develop drugs for the treatment of WAS. The primers and probes can be used in genetic analysis. The antibodies are used to detect the WAS
                     GVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPGIRP 439
                                                                                                   SSPVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKR-HPSTLPVISDAR 498
                                                         ------ 391
                                                                                                                                                                                                           177 RK------QKQKNLDRPHEPEKVPRAPHDRRREWQKLAQGPEL-----AEDDAN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 npgrsyflrifdikdgkllwegelynnfvynsprgyfhtfagdtcqvalnfaneeeakkf 127
                                                                                                                          499 SVLLEAIRKGIQLRKVEEQREQ----EAKHERIENDVATILSRRIAVEYSDSEDDSEFDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neural-Wiskott-Aldrich syndrome protein; N-WASP; haemmorhage; Wiskott-Aldrich syndrome; WAS; eczema; recurrent infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Neural-Wiskott-Aldrich syndrome protein - used pharmaceuticals for the treatment of this syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 NP--SYF---FD------LWKEKMLQD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat Neural-Wiskott-Aldrich syndrome protein.
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Matches 129; Conservative
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                                                         369 gpvappppp---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           raptaapppppps----rpsvevppppnrmyppppalpssapsgpppppsvlgv 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HDRRREWQKLAQGPELAEDD----ANLLHKHIEVAN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PPPPLPSALSTSSLRASMTSTPPPPVPP-PPPPPATALQAPAVPPPPAPLQIAP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 avknelrrqapppppsrg-gpppppppppssgp----ppppargrg---appppps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 GPASHFETRPQTYVD-----HMDGSYSLSALPFSQMSELLTRAEERVL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Neural-Wiskott-Aldrich syndrome protein – used to develop
pharmaceuticals for the treatment of this syndrome
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                                                                                                                                                                                                                                                                                     Neural-Wiskott-Aldrich syndrome protein; N-WASP; haemmorhage; Wiskott-Aldrich syndrome; WAS; eczema; recurrent infection;
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                                                                                                                                                                                                                                             Human Neural-Wiskott-Aldrich syndrome protein.
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(TAKE/) TAKENAWA T.
                                                                                                                    W46889 standard; Protein; 505
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          Query Match
Best Local Simi
Matches 135;
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ishtkekkkgkakkkrltkadigtpsnfqhighvgwdpntgfdlnnldpelknlfdmcgi
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                                                                                                                                                                                                                     412 VHPLPQGEVQGLPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLMP
                                                                                                                                                                                                                                            -----pppppppppppgl-----psdgdhqvpass-gnkaall-
                                                                                                                                                                                                                                                                   472 PSPPSQVIPASEPKR-HPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQ----EAKHER
                                LLH-------KHIEVAN-GPASHFE-----TRPQTYVD-----HMDGSYSLSAL
                                                                               ---VRPHEPPPPPPMHGAGDAKPIPTCISS
                                                                                                                                                                         PP-PPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVP
                                                                                                                                                                                               338 rmypppppalpssapsgpppppplsma-gstappppp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-Wiskott-Aldrich syndrome protein; N-WASP; actin polymerisation; bone structure formation.
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                                                                                                                                                                                                                                                                                                                               527 IENDVATILSRRIAVEYSDSEDDSEFDEVDW 557
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                                                                              PFSQMSELLTRAEERVL-
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                                                                                                                                                                                                                                                                                                                              306 grgapppppsra--ptaapppppsr--pgvgappppprrmypp---plpalpssap--- 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVPVHPLPQGEVQG-LPPPPPPPPPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHV 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...-repppppphs-----30ppppar 305
                                                                                                             65
                                                                                                                                                                                                                                                     6 ggpppprrvtnvgsllltpgeneslftflgkkcvtmssavvglyaadrncmwskkcsgva
                                                                                                                                                                                                                                                                                                      200 RRREWQKLAQGPELAEDD----ANLLHKHIEVANGPASHFETRPQTYVD-----HMDGS
                                                                                                                                                                                                                                                                                                                                                                               250 YSLSALPFSQMSELLTRAEERVL------VRPHEPPPPPPMHGAGDAKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPBALSTSSLRASMTSTPPPPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 -- PPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPP--IAPPLVQPSPPVARAAPVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 sgpppppplsvsgsvappppppppppg--pppppgl----psdgdhqvptpa-gska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLMPPSPPSQVIPASEPKR-HPSTLPVISDARSVLLEAIRKGIQLRKVEEQREQ----EA
                                   229;
 Length
 Score 332.5; DB 19; Length
Pred. No. 1.7e-14;
; Mismatches 145; Indels
                                                                        129 EQPPPLN-----ILTPYRDD-----GKE-----GLKFYT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   523 KHERIENDVATILSRRIAVEYSDSEDDSEFDEVDW 557
                                                                                                                                                                                                                           172 KRKEKRK-----QKQKNLDRPHEPEKVPRAP-
                                                                                                                                                   153 ----NP--SYF---FD-----LWKEKMLQD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mDia Rho targeting protein.
                                     :99
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11.2%;
ilarity 23.5%;
Conservative 6
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target
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                                                                       Mus sp.
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                                                                                                                                                                                                                                                                               34;
                                                                                                        diaphanous). This protein has active type Rho protein-combining ability, has proline-combining ability, has a M.W. of 150 KDa measured by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and its gene is positioned at human chromosome 5q31.2. The nucleic acid can be used for the recombinant production of the protein. The protein is useful for the elucidation of mechanism of diseases such as respiratory tract oversensitiveness, bronchial asthma, acute marrow leukaemia and marrow
                                                                                                                                                                                                                                                                                                                       360 linalitpaeeldfrvhirselmrlglhqvlqdlreienedmrvqlnvfdeggeedsydl 419
                                                                                                                                                                                                                                                                                                                                                                                                   185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----dsgtiippppapgdsttpp-ppppppppppppggvcisspps1pggtai 682
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                                                                                                                                                                                                                                                                                                                                                                           420 kgrlddirmemddfnevfg-----illntvkdskaephflsilghlllvrndye 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPPPP-----VPPPPP-PPATALQAP-----AVPPPPAPLQIAPGVLHPAPPPIAPP 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lpgsagippppp------plp-gea-gmpppppplpggpgippppfpggp- 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTALAHPPSGLHPTPSTAPGPHVPLMPP----SPPSQVIP-ASEPKRHPSTLPVISDAR 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    814
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                                                                                               (mammalian
                                                                                                                                                                                                                                                                                                     91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDGSYSLSALPFSQMSELLTRAEE------RVLVRPHEP----PPPPPMHGAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L----VQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPP----PPLPPPGIRPSSPV
                                   of
                                                                                                                                                                                                                                                                                                     51 IFGELFNEAHSFSFRVNSLQERV------DRLSVSVTQLDPKEEELS-
                                                                                                                                                                                                                                                                             193;
                                   yet protein and its gene - useful for elucidation respiratory tract disease
                                                                                                                                                                                                                                                       Length 1315;
                                                                                               mDia
                                                                                                                                                                                                                                                                             183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----gipppp---pgmgmpppppfgfgvpaapvlpfgltpkk
                                                                                              sequence represents a human Rho target protein,
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----lykpevglrrpnwsklvaedlsgdcfwtkvkedrfenn 852
                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                                                  Pred. No. 3e-13
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                       .10.8%; Score 320.5;
                                                                     Claim 2a; Page 28-31; 54pp; Japanese.
                                                                                                                                                                                                                                                                             59;
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                                                                                                                                                                                                                                                                 25.4%;
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                                                                                                                                                                                                                                                                  Best Local Similarity 25.4
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W52249 standard; Protein;
1999-002481/01
                                                                                                                                                                                                                   1315 AA;
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                                    target
           N-PSDB; V62933
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mechanisms of
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                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454
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                                                               activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - useful for, e.g. reconstituting actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLDRPHEPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 VPRAPHDRRREWQKL-----AQGPELAEDDANL-----LHKHIEVANGPASH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lskeledaknemaslsavvvapsvsssaavppapplpgdsgtvipp--ppppppppp---
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                                                            et protein; p140mDia; mouse; Rho protein combining ac combining activity; inhibitor; actin cell structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 18-23; 28pp; Japanese
Mouse Rho target protein p140mDia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rho target protein p140mDia cell structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIRI ) KIRIN BREWERY
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Matches 138; Conserv
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455 LHPTPSTAPGPHVPLMPPSPPSQVIPASEP----KRHPSTLPVISDARSVLLEAIRKGIQ 510
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                                                                                                                                    542 lskeledaknemaslsavvvapsvsssaavppapplpgdsgtvipp--pppppplpg---
                                                                                                                                                                                                                                                                                  346 STPPPP-----VPPPPPPPATALQAPAVPPPPAPLQIAPGVLHPAPPPIAPPLVQPSP
                                                                                                                                                                                                                                                                                                                                                                             399 PVARAAPVCETVPVHPLPQGEVQGLPPPPPPPP----LPPPGIRPSSPVTVTALAHPPSG
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---AQGPELAEDDANL-----LHKHIEVANGPASH
                                            484 tar--helgvemkkmendfegklgdlggekdaldsekggitagkgdleaevskltgevak
                                                                                          235 FETRPQTYVDHMDGSYSLSALPFSQMSELLTRA-----EERVLVRPHEPPPPPPMHGAGD
                                                                                                                                                                                       290 AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPP----PPPPPLPSALSTSSLRASMT
                                                                                                                                                                                                                                    597 -----gvv---gvv---ppsp------plppgtcippppplpgg-----a
                                                                                                                                                                                                                                                                                                                              622 cippppglpgsaaippppplpgva---sipppp-plpgatai--ppppplpgataippp
                                                                                                                                                                                                                                                                                                                                                                                                                            675 p-----plpgg--tgippppplpgsvgvppppplpggp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculosis; mycobacteria; infection; diagnosis;
antimycobacterial; antibiotic; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis 55 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 LRK-----VEEQREQE-----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W31855 standard; Protein; 572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 16; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moreno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-EP01973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
  193 VPRAPHDRRREWQKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Espitia C, Honisch C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-549750/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T93610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a mouse Rho target protein, mDia (mammalian diaphanous) which is used in a method to extract a human mDia protein. This human protein has active type Rho protein-combining ability, has proline-combining ability, has proline-combining ability, has a M. of 150 KDa measured by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and its gene is positioned at human chromosome 5q11.2. The nucleic acid can be used for the recombinant production of the protein. The protein is useful for the elucidation of mechanism of diseases such as respiratory tract oversensitiveness, bronchial asthma, acute marrow leukaemia and marrow
                                                                                                                                                                                                                                                                                                                                                                                                                  Rho Protein; mDia; mammalian diaphanous; target protein; murine; Rho protein-combining; prolline-combining; chromosome 5q31.2; disease; respiratory tract; oversensitiveness; bronchial asthma; marrow leukaemia; marrow dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | |||: | |||308 linalitpaeeldfrvhl---rselmrlglhqvlqelreienedmkvqlcvfdeq-gded 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 IFGELFNEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 LFDRK-----YRDDGKEGLKFY- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLDRPHEPEK 192
Score 318.5; DB 20; Length 1255;
Pred. No. 3.9e-13;
64; Mismatches 192; Indels 177; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Rho target protein and its gene - useful for elucidation of mechanisms of respiratory tract disease
                                                                    511 LRK-----VEEQREQE-----AKHERIEND 530
                                                                                             Example 4; Page 19-22; 54pp; Japanese.
                                                                                                                                                                                                                                 W76733 standard; Protein; 1255 AA
                                                                                                                                                                                                                                                                                                                                                                          Mouse mDia Rho targeting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.78;
24.28;
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Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KIRI ) KIRIN BREWERY KK
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N-PSDB; V62932.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP10262680-A.
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                                                                                                                                                                                                                                                                                W76733;
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                                                                                               13;
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                                                                                                                                                      LIENRP-QSPATGRTPVFVSPTPP-PPPPLPSALSTSSLRASMTSTPPPPPPPPPA 360
                                                                                                                                                                 QGEVQGLPPPPPP-----PPLPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLM 470
                                                                                                                                                                                                                                                    274 psekpnppappeppepksspalppappapsmpsavrvppspp--ippappaaprasmpal 331
                                                                                                Gaps
            for
                                                                                                                                                                                           TALQAPAVPPPPAPLQI.APGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHP----LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This novel 74 kDa protein is encoded by an open reading frame of a Mycobacterium tuberulosis DNA fragment (see T93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known
and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, i monitoring vaccination, and for the development of vaccines and
                                                                                               77;
                                                                             Length 572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                               89; Indels
                                                                                                                  ---TCISS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA and related proteins or RNA derived from M.
                                                                                                                                                                                                                                                                                     332 ppappsppatrlcpplppsppappappappapptppkllsa 372
                                                                                                                                                                                                                                                                       PPSPPS-----QVIPASEPKRHPSTLPVISDARSVLLEA 504
                                                                             DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                infection; diagnosis;
                                                                           10.7%; Score 317.5; DB 1
33.8%; Pred. No. 1.9e-13;
iive 20; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Singh M;
                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis 74 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          antimycobacterial; antibiotic; vaccine
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                                                                                                                                                                                                                                                                                                                                      W31852 standard; Protein; 763
                                                                                                                 275 PHEPPPPPMHGAGDAKPIP---
                                                                                                                                                                                                                                                                                                                                                                                                                Tuberculosis; mycobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-EP01973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96DE-4017184
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                              anti-mycobacterial drugs.
                                                                                     l Similarity 33.8
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Honisch C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 13; 55pp;
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                                               572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T93610.
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                                                 Sequence
                                                                             Query Match
                                                                                       Best Local
Matches 9
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pnshppapp-----sapvpgvplaplpisgrpvsvwkgsfttlstfccrvcsgevlaga 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIENRP-QSPATGRTPVFVSPTPP-PPPPPLPSALSTSSLRASMTSTPPPPVPPPPPA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       talappl--pplaplpispgv--ppappippgkpwttpplapappepktvpvlppgpscp 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGEVQGLPPPPPP-----PPLPPPGIRPSSPVTVTALAHPPSGLHPTPSTAPGPHVPLM 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psekpnppappeppepksspalppappapsmpsavrvppspp--ippappaaprasmpal 522
                                                                                                                                                                                                                                                                                                                     77; Gaps
              Proteins (see Wil851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and anti-mycobacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TALQAPAVPPPAPLQIAPGVLHPAPPPIAPPLVQPSPPVARAAPVCETVPVHP----LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human diaphanous polypeptide useful in general diagnosis and
                                                                                                                                                                                                                                                                          DB 18; Length 763;
  tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Welcsh PL;
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                                                                                                                                                                                                                                                                                                                                                                     ---TCISS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 PPSPPS-----QVIPASEPKRHPSTLPVISDARSVLLEA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ppappsppatrlcpplppsppapnsppappapptppkllsa 563
                                                                                                                                                                                                                                                                        ; Score 317.5; DB 18;
; Pred. No. 2.6e-13;
20; Mismatches 89;
  Novel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morrow JE,
of mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lynch ED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (Dial).
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                                                                                                                                                                                                                                                                          10.7%;
33.8%;
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97US-0063737
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                                                                                                                                                                                                                                                                                                                          Conservative
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N-PSDB; X55568.
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                          763 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human diaphanous
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                                                                                                                                                                                                            Sequence
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173
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                                                                                                                                                                 34;
 This represents a recombinant human diaphanous polypeptide (Dial), having diaphanous-specific amino acid sequence and bioactivity. The polypeptide is useful for screening for agents that modulate binding of human diaphanous polypeptide to a binding target. The modulators are useful for stabilizing actin filaments. Probes and primers of the nucleic acid are useful for diagnosis of conditions, and as immunogens, reagents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446
                                                                                                                                                                                                                                                            290 AKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPPPPPPPPPPPSALSTSSLRASMTSTPP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      675
                                                                                                                                                                                                                                                                                                                                              245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621
                                                                                                                                                                                                                  308 linalitpaeeldfrvhirselmrlglhqvlqdlreienedmrvqlnvfdeqqeedsydl 367
                                                                                                                                                                                                                                         92 ---LQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYDVCEQPPPLNILTP---YRDDGK 145
                                                                                                                                                                                                                                                                                           146 EGLKFY------TNPSY---FFDLWKEKMLQDTEDKRK-EKRKQKQKNLD 185
                                                                                                                                                                                                                                                                                                                    417 arpgyyklieecisgivlhkngadpdfkcrhlqieieglidgmidktkvekseakaaele 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 ALAHPPSGLHPTPSTAPGPHVPLMPP----SPPSQVIP-ASEPKRHPSTLPVISDARSVL 501
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              186 RPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQTYVDH
                                                                                                                                                                                                                                                                                                                                                                                             246 MDGSYSLSALPFSQMSELLTRAEE-----RVLVRPHEP----PPPPPMHGAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PP----VPPPPP-PPATALQAP-----AVPPPPAPLQIAPGVLHPAPPPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pplsgdatippppplpegvgipspsslpggtaipppp-pl---pgsaripppp--pplpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 sagippppp-----plp-gea-gmppppppppggpgppppppppppppppgp----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:-VQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPP----PPLPPPGIRPSSPVTVT
                                                                                                                                                                                                                                                                                                                                                                    kkldseltar--helqvemkkmesdfeqklqdlq-----gekdalhse-kqqiatek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----dsgtilppppapgdsttpp-pppppppppppppgtais-----pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; atrophin-1 related protein; Charcot-Marie-Tooth disease;
Schwartz-Jampel syndrome; crystalline corneal dystrophy;
dentatorubral pallidoluysian atrophy; ataxia.
                                                                                                                                          DB 20; Length 1248;
                                                                                                                                                                                          --DRLSVSVTOLDPKEEELS-
                                                                                                                                                                 Indels 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 313.5; DB 20;
; Pred. No. 8.3e-13;
58; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 LEAIRKGIQLRK-----VEEQREQE-----AKHERIEND 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      751 --lykpevglrrpnwsklvaedlsgdcfwtkvkedrfenn 788
                                                                                                                                                                                         51 IFGELFNEAHSFSFRVNSLQERV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y17406 standard; Protein; 1012 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human atrophin-1 related protein.
                                                                                                                                       Query Match
Best Local Similarity 25.2%;
Matches 146; Conservative 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                    1248 AA;
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atrophin-1 related general.

attrophin-1 related general.

agonists of (II) are used to treat or prevent conditions requiring an agonists of (II) are used to treat or prevent conditions requiring an (III), inhibitory nucleic acid and/or competitive polypeptides are used to treat conditions requiring reduced activity or expression of (II). Typical of these conditions are Ohnsoch Marie-Tooth disease;

Schwartz-Jampel syndrome; crystalline corneal dystrophy, dentatorubral pallidoluysian atrophy and ataxia. These diseases, or susceptibility to them, can be diagnosed by detecting mutations in (II)-encoding genes and/or by measuring levels of (II). Cells that express (II), or their membranes, can be used to screen for specific (ant)agonists, potential that appears of (II), or its fragments, are used as probes to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related sequences; as reagents for research, diagnosis and drug screening; for chromosome identification; and for expressing recombinant (II). (II) and their fragments, are used to raise specific antibodies (useful for isolation and identification of (II)-expressing clones, for purification of (II), as therapeutic antagonists, as assay reagents and in drug screening); in vaccines; to screen for (ant)agonists and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 NSLQERVDRLSVSVTQLDPKEEELSLQDITMRKAFRSSTIQDQQLFDRKTLPIPLQETYD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 ssgrnspsaastssndskaetvkksakkvkeeassllksnkrg····rekvasdteead 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 rtsskktktgeisrpnspsegegessdsrs-----vndegssdpkdidgdnrst 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PPLVQPSPPVA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKEKRKQKQKNLDRPHEPEKVPRAPHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 LRASMISIPPPPVPPPPPPATALQ------AP--AVPP-----PPAP--LQIAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents human atrophin-1 related
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human atrophin-1 related gene and polypeptide useful for Charcot-Marie-Tooth disease and Schwartz-Jampel syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Mismatches
                                                                                                                                                                                                                                                                     Xia J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PIA-
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                                                                                                                                                                                                                                                                     Wang
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23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 25-27; 34pp;
                                                                    97WO-CN00108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identify specific receptors
                                                                                                                                  97WO-CN00108
                                                                                                                                                                                                   HUNAN MEDICAL.
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                                                                                                                                                                                                                                                                     Ruan Q,
                                                                                                                                                                                                                                                                                                                               WPI; 1999-326701/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; X56436
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                                                                                                                                                                                                   (UYHU-) UNIV
                                                                    27-OCT-1997;
                                                                                                                                      27-OCT-1997;
06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154;
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                                                                                                                                                                                                                                                                     Deng H,
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29;

27;

Indels 240; Gaps

Mismatches 138;

36;

Conservative

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Matches 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arginine methylation; arginine methyltransferase activity; mouse; Wiskott-Aldrich syndrome; antibody; SLM-1; SLM-2; WASP; hnRNP K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assaying arginine methyltransferase activity useful for determining whether a cell is cancerous or has cancer potential comprises measuring the methylation of specific substrates such as SLM-1, SLM-2, Sam68
                                                                                                                                                                                                                               488
309 lqhpgppqpfglppqasqgqaplgtspaaayphtslqlpasqsalqsqqppreqplppap 368
                                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                             489 gpppitpptcpststppagpgtsagppcsgaaasggsiaggsscplptvgikeealddae 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 epespppprspspeptvvdtpshasgsarfykhldrgynscartdlyfmplagsklakk 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a novel method for assaying arginine
                                                                                            | | | : | | ||||
369 lamphikpppttpipqlpapgahkhpphlsgpspfsmnanlppppalkplsslsthhpps
                                                                                                                                                                         --PPP-----PLP----PPGIRPSSPVTVTALAHPPSGLH---PTPSTA-----PG
                                                                                                                                                                                                                               429 ahppplqlmpqsqplpsspaqppgltqsqnlppppashptglhqvapqppfaqhpfvpg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER
                                                           ------GENOG-----
                                                                                                                                                                                                                                                                                                                                                                                                     EPK-----RHPSTLPVISDARSVLLEAIR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B49336 standard; peptide; 520 AA.
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                                                        402 RAAPVCETVPVHPLPQ-
                                                                                                                                                                                                                                                                                       465 PHVPLMPPSPPSQVIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 EEQREQEAKHE 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 reealekakre 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine WASP protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richard S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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Length 520;

Score 297; DB 22; Pred. No. 3.9e-12;

10.0%; 24.3%;

Query Match Best Local Similarity

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuperssant; cardiant; immunostimulant; thrombolytic; cogqulant; vasotropic; autidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCDE; ALDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antlinflammatory disease; coagulation;
QETYDVCEQPPPLNILTPY-----RDDGKEGLKF--YTNPSYFFDLWKEKMLQDTEDKRK 174
                                                                                                                                                                                                                                    HMDGSYSLSALPFSQ--MSEL-LTRAEERVLV-------RPHE--PPPPP 282
                                                                                                                                                                                                                                                                                                                                       : | :| ||: :|| || || ||: 262 unnldpdlrsl-fsragiseaqltdaetskliydfiedqggleavrqemrrqeplppppp 320
                                                                                                                                                                                                                                                                                                                                                                                                                PMH-----GAGDAKPIPTCISSATGLIENRPQSPATGRTPVFVSPTPP---- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 -PPPPPLPSALSTSSLRASMTSTPPPP---VPPPPPPPATALQAPAVPPPPAPLQIAPGV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 gapppptprg------ppppgrggppppppatgrsgp--pppplpgaggp-- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 LHPAPPPIAPPLVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPPPPPGIRPSS 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       grqsgerrqlppppapineerrgglppvpphpggdhggpsggplslglvtvdignpdits 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 PVTVTALAHPPSGLHPTPSTAPGPHVPLMPPSPPSQVIPASEPKRHPSTLPVISDARSVL 501
                                                                                                                                                                                                      -----APHDRRREWQKLAQGPELAEDDANLLHKHIEVANGPASHFETRPQTYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------pcpgsgpap----pplpptpvsggs----papgggrgal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAIRKGIQLRKVE---EQREQEAKHERIENDVAT---ILSRRIAVEYSDSE-----DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ORFX ORF2828 polypeptide sequence SEQ ID NO:5656.
                                                                                                      EKRKQKQKNLDRPHEPEKVPR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B43064 standard; Protein; 987 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEFDEVD 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513 eeddewd 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200058473-A2
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PR 31-MAR-1099; 99US-0127607.

PR 02-APR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 03-APR-1999; 99US-0127636.

PR 03-APR-1999; 99US-0127636.

PR 03-APR-1999; 99US-0127636.

PR 03-APR-2000; 2000US-0540763.

PR 03-MAR-2000; 2000US-0540763.

PR 04-PEDB 05-2000US-0540763.

AX WPI; 2000-602362/57.

PR Novel nucleic acids and peptides derived from open reading frame X, PT usurodegenerative disorders and cardiovascular disease - CC ardiant; thrombolytic; coaquiant; vasotropic; neuroprotective; ontribancerial; antifungal; antifu
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382 hgvvsspyvgvgpappvaglpsapppqfsgpelamavrpatttvds-igapipshtaprp 440 91 SLQDITMRKAFRSSTIQ------DQQLFDRKTLPIPLQETYDVCEQPPPLNILTP 139 162 aaqdrvl-calteanvqyaavrrvlsdldqkwnstlqtlvasyeaye-----d 208 140 YRDDGKEGLKFYTNPSYFFDLWKE--KMLQDTEDKRKEKRKQKQKNLDR--PHEPEKVPR 195 209 lmkksqegrdfya----dleskvaallertgstcqareaarqqlldrelkkppprpt 262 196 APH---DRRREWQ-----KLAQGPELAE---DDANLLH---KHIEVANG 230 263 apkpllprreeseaveagdppeelrslppdmvagprlpdtflgsatplhfppspfpsstg 322 231 PASHFETRP------QTYVDHMDGSYSLSALPFSQMSELLTRAEERVLVRPHEPP- 279 323 pgphylsgplppgtysgptqliqprapgphampvapgpalypapaytpelglv-prsspg 381 280 ------PPPPMHGAGDAKP-----IPTCISSATGLIENRPQSPATGRTPVFV 320 Indels 165; Gaps 32 ISLANIIRQLSSLSKYAEDIFGELFNEAHSFSFRVNSLQ-ERVDRLSVSVTQLDPKEEEL 90 Query Match 9.7%; Score 289.5; DB 21; Length 987; Best Local Similarity 24.6%; Pred. No. 2.5e-11; Matches 142; Conservative 55; Mismatches 215; Indels 165; g g qq g ð 셤 õ ð ò à ð

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Qy	321	321 SPTPPPPPPPPLPSALSTSSLRASMTSTP	D.
QQ	441		0
οy	356	356 PPPPATALQAPAVPPPAPLQIAPGVLHP-APPPIAPPLVQPSPPVA 401	_
QQ	501	501 qphpsqaf-gpqpppqqplplqhphlfppqapgllppqspypyapqpgvlqqppplhtql 559	6
Qy	402	402 RAAPVCETVPVHPLPQGEVQGLPPPPPPPDPPPGIRPSSPVTVTALAHPPSG 454	4
Dp	260	ypgpaqdplpahsgalpfpspgppqpphpplaygpapstrpmgpqaapltirgpss 615	S
, o	455	455 LHPTPSTAPGPHVPLMPPSPPSQVIPASEP 484	
qa	919	616 aggstpsphlypspapspgpypprppaaep 647	

Search completed: June 20, 2001, 12:07:35 Job time: 50 sec

12 20 0.8 1201 21 A62524 13 20 0.8 1428 21 A99466	20 0.8 3435 17 T35869 Human DNA po 20 0.8 4371 21 A99469 Sakuranetin 20 0.8 5241 21 A99467 Sakuranetin	19 0.7 300 · 20 213606	19 19 0.7 504 15 119877 Human gene Sign 20 19 0.7 826 20 V99893 Fragment of asp 21 19 0.7 927 19 V29596 Humicola insole	19 0.7 1250 19 0.37483 19 0.7 1257 19 0.13840 19 0.7 1506 19 0.16721	19 0.7 1590 19 V27169 19 0.7 1736 21 298322 19 0.7 1737 20 X95508	29	32 19 0.7 2111 17 33 19 0.7 2111 19	19 0.7 2111 21 A38401 19 0.7 2181 12 014967 19 0.7 2352 20 X87656	38 19 0.7 17341 21 A14872 39 19 0.7 23449 21 235393	40 18 0.7 24 17 139968 41 18 0.7 24 19 V55816		ALIGNMENTS	RESULT 1 061275/c ID Q61275 standard; DNA; 359 BP.	XX XX Q61275;	DA 16-MAR-1994 (first entry)	Human brain Expressed Sequence Tag EST01293.	KW Gene transcription product; genetic markers; tagging; in vivo; KW transcription; mapping; locations; chromosomes; chromosomal; ss. XX	OS Homo sapiens. XX PN WO9316178-A.	XX PD 19-AUG-1993.	XX PF 12-FEB-1993; 93WO-US01294.	AX PR 12-FEB-1992; 92US-0837195.	AA (USSH) US DEPT HEALTH & HUMAN SERVICE. XX	-	DR WPI; 1993-272882/34	PT Enriched oligonucleotides and corresp. sequences - used as . PT markers for human genes transcribed in-vivo, facilitate tagging PT of most human genes	Example
GenCore version	Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: June 20, 2001, 19:41:43 ; Search time 172.72 Seconds (without alignments) 8872.313 Million cell updates/sec	Tille: Perfect score: 2625 Sequence: 1 cttctcttgcacttgcggataatggttcattttaaaagtt 2625	able: OI Ga	Searched: 678276 seqs, 291890651 residues	0	iotai number oi nitš satisiying chosen parameters: Minimum DB seg length: 0 Maximum DB seg length: 0	cessing: Listi	N_Geneseq_0401:*	H 0 W 4 L	5: /SIDSZ/gcgdata/geneseq.geneseqn./Mal985.Dar:* 6: /SIDSZ/gcgdata/geneseq/geneseqn/Nal985.Dar:* 7: /SIDSZ/gcgdata/geneseq/geneseqn/Nal987.Dar:* 8: /SIDSZ/gcgdata/geneseq/geneseqn/Nal987.Dar:*	/SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT	13: /SIDSZ/gcgdata/geneseq/geneseqn/NA1991.DAT:* 14: /SIDSZ/gcgdata/geneseq/geneseqn/NA1991.DAT:*	17. /SIDSZ/gogdata/genescq/yenescqn/Na1995.hr. 16. /SIDSZ/gogdata/genescqn/Na1995.hr.* 17. /SIDSZ/gordata/cenescqn/na1996.hr.*	18: /SIDSZ/gcgdata/geneseqn/Na1997.DAT:* 19: /SIDSZ/gcgdata/geneseqn/Na1997.DAT:*	20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:* 21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:* 22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*	즉	of the total score distribut		result No. Score Match Length DB ID Description	254 9.7 359 14 177 6.7 242 21	110 4.2 165 21 C17657 HUMAN 23 0.9 359 21 A43416 Rat se	22 0.8 400 21 C10511 22 0.8 400 21 243075	7 22 0.8 1583 21 293303 Sequer 8 22 0.8 2295 21 288238 Human 9 21 0.8 1203 21 C36419 Arabic	21 0.8 3070 21 A26364 21 0.8 4021 21 C77217

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LaVallie ER, Collins-Racie LA,

Treacy M; McCoy JM,

Jacobs K, Mu

(GEMY) GENETICS INST

99WO-US24205. 98US-0104435

15-OCT-1999;

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            The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST01293 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also 059041-061440.
                                                                                                                                                                                                                                                                                                              2376 cttgtagtgttgaattctcttaaaggaatgcttgaattttttcattattgtttattgtt 2435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2496 gatatgattttgcttgcctataggagttaaaaacttttccatgtgaaatactctgactta 2555
                                                                                                                                                                                                                                                                                                                                                                                   2316 atgittiaaaagaagaagaacactgccttgattatacgaatacactcagaaagtacatttag 2375
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                            Query Match 9.7%; Score 254; DB 14; Length 359; Best Local Similarity 99.4%; Pred. No. 2e-112; Matches 354; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                         Sequence 359 BP; 137 A; 57 C; 55 G; 110 T; 0 other;
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Human secreted expressed sequence tag SEQ ID NO:1368.
   A42628 standard; cDNA; 242 BP
                   21-AUG-2000 (first entry)
           A42628;
A42628
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Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; harding to the consideration analysis; antidiamentopoietic; chemokinetic; antibacterial; antifungal; antiviral; antidiamentory; cytostatic; antibacterial: antifungal; antiviral; antidiamentory; cytostatic; unnerary; antiparkinsonian; antiviral; antidiamentory; cytostatic; unnerary; antiparkinsonian; antiviral; auticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coaqulation disorder; hammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.

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WO200021990-A1
                         20-APR-2000
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Homo sapiens

Ad1261 to Ad3419 represent specifically claimed secreted expressed
sequence tags (sESTs) isolated from human, mouse, xenopus and rat
tissues sources. The sESTs can have a range of activities depending on
the tissues they were isolated from. The activities depending on
the tissues they were isolated from. The activities include: chemotactic;
broliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
chemostatic; thrombolytic; antinflammatory; cytostatic; antibacterial;
chemostatic; thrombolytic; antinflammatory; cytostatic; antibacterial;
cartifungal; antiviral; antidiabetic; antibarhmatic; vulnerary; antiulcer;
cartifungal; neuroprotective; nocropic; antiparkinsonian; antipsoriatic;
cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
used for gene therapy and in vaccines. The sESTs are useful as probes for
the identification and isolation of full-length cDNAs and genomic DNA
molecules which correspond to the sESTs. Proteins encoded by the sESTs
are useful in assays for determining blological activity and raising
antibodies. They may be useful for treatment of autoimmune disorders;
(multiple sclerosis, insulin dependent diabetes), allergic conditions
of seteoporosis, osteoarthritis, central nervous system disorders
(hazheimer's, parkinson's, Huntington's disease, stroke), coagulation
disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
disease), tumours, bacterial, fungal or viral infections, depression
and psoriasis. Ad3420 to Ad3425 represent linker variants which are
in the exemplification of the present invention. Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autolmmune, infectious, and central nervous system disorders \cdot Sequence 242 BP; 83 A; 52 C; 65 G; 42 T; 0 other; Claim 1; Page 450; 618pp; English. WPI; 2000-317937/27.

0; Gaps Query Match 6.7%; Score 177; DB 21; Length 242; Best Local Similarity 100.0%; Pred. No. 2.5e-75; Matches 177; Conservative 0; Mismatches 0; Indels 0

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BP

C17657 standard; cDNA; 165

RESULT C17657 C17657;

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss. Human secreted protein 5' EST, SEQ ID NO: 21732. 06-OCT-2000 (first entry)

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The present sequence is one of a large number of 5 ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5 ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3 untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5 ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5 UTR is rarely included 5 ESTs are derived from mRNAs with intext 5 ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5 ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; antibaesic; haemostatic; thrombolytic; antiinfammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; antidiabetic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTS and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat secreted expressed sequence tag SEQ ID NO:2156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 165 BP; 43 A; 48 C; 25 G; 49 T; 0 other;
                                                                                                                                                                                                                                                 Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 21732; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                 Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression and secretion vectors,
                                                                                                                               21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                     99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A43416 standard; cDNA; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2000 (first entry)
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Matches 110; Conserv
                                                                                                                                                                                                           (GEST ) GENSET
                                                     EP1033401-A2.
                   Homo sapiens
                                                                                                                                                                     26-FEB-1999;
                                                                                           06-SEP-2000
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A43416
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proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antinflammatopy; cytostatic; antibacterial; antifundabetic; antibathmatic; vulnerary; antibucer; osteopathic; neuroprotective; notropic; antiparkinsonian; antibacterial; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTS can be used for gene therapy and in vaccines; The SESTS are useful as probes for the identification and isolation of full-length coNAs and genomic DNA molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, antibodiess), and the sclerosis, parking the sclerosis, parking the sclerosis, parking the sclerosis, parking the sclerosis and the scentral nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A41261 to A43419 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, xenopus and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTS), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. A43420 to A43425 represent linker variants which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                central nervous system disorder; Alzheimer's disease; stroke;
Parkinson's disease; Huntington's disease; coagulation disorder;
haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
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lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
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100.0%; Pred. No. 0.39;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                       Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 359 BP; 75 A; 131 C; 83 G; 70 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein 5' EST, SEQ ID NO: 14586.
                                                                                    tumour; infection; depression; psoriasis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 612-613; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1785 gaagagcagcgtgaacaggaagc 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 gaagagcagcgtgaacaggaagc 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C10511 standard; cDNA; 400 BP
                                                                                                                                                                                                                                                                    99WO-US24205
                                                                                                                                                                                                                                                                                                                98US-0104435
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                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-317937/27.
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                                                                                                                                                                               WO200021990-A1
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Best Local Similar
                                                                                                                                                                                                                                                                      15-0CT-1999;
                                                                                                                                                                                                                                                                                                                15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-0CT-2000
                                                                                                                                                                                                                            20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                       Jacobs K,
Merberg D,
                                                                                                                                   Rattus sp.
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C10511
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Duclert A, Giordano J;

99WO-IB00712. 98US-0057719.

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Novel secreted protein 5' expressed sequence tag sequences used in diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                        Dumas Milne Edwards J,
                                                                                                                                WPI; 2000-038446/03.
                                                                              (GEST ) GENSET
             09-APR-1999;
                                      09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
          Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification; ss.
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Pred. No. 1.2;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 5' EST isolated from a cDNA library SEQ ID NO:1622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 400 BP; 106 A; 111 C; 110 G; 70 T; 3 other;
                                                                                                                                                                                                         Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 14586; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.8%; Scur
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z43075 standard; cDNA; 400 BP
                                                                                                                               21-FEB-2000; 2000EP-0200610
                                                                                                                                                          99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                             Dumas Milne Edwards J,
                                                                                                                                                                                                                                       WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                    (GEST ) GENSET
                                                    Homo sapiens.
                                                                           EP1033401-A2
                                                                                                                                                         26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09953051-A2
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                                                                                                      06-SEP-2000
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sequences, corresponding to human secreted proteins. Y64651 to Y65438 sequences, corresponding to human secreted proteins. Y64651 to Y65438 represent the EST-related proteins corresponding to Z4265 to Z43052.

The 5' ESTS can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTS are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTS can also be used in forensic procedures to identify individuals, or in diagnostic procedures to chentify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. Z4224 to 24224 and Y64644 to Y64650 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homer; calcium; receptor; immediate early gene; IEG; identification; treatment; glutamate receptor; inositol triphosophate; epilepsy; glutamate toxicity; memory disorder; learning disorder; stroke; schizophrenia; Alzheimer's disease; tissue degeneration; brain development; cardae disorder; mescular disorder; recological disorder; psychiatric disorder; renal disorder; uterine disorder; bronchial disorder; ageing; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242264 and Y64644 to Y64650 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding human homer interacting protein 130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 400 BP; 106 A; 111 C; 110 G; 70 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%; Score 22;
100.0%; Pred. No.
ative 0; Mismatc
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160..1120
Claim 1; Page 837; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1075 cacctccacctccactgca 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 cacctccacctccaccaatgca 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z93303 standard; DNA; 1583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ношо
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Identifying compounds capable of modulating cellular response useful for treating Alzheimer's disease and cardiac disorders, involves incubating compound with cell expressing Homer protein and cell-surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homer proteins are the products of neuronal immediate early genes (IEG's). They selectively bind the carboxy termini of certain cell-surface receptors, certain intracellular receptors and binding proteins. Many forms of Homer proteins contain a "coiled-coil" structure in the carboxy terminal domain which mediated homor and heteromultimerisation between Homer proteins. Homer plays a significant role in mediating receptor-activated calcium mobilisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal, uterine and bronchial tissue disorders and for affecting the natural aging process. These compounds are also useful for modulating receptor-mediated calcium mobilization, by exposing a cell to the compound to modulate calcium mobilization that normally occurs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from intracellular stores. Thus, cells expressing a Homer protein can be used to identify a compound capable of modulating a cellular response mediated by cell surface receptor or intracellular receptor. Compounds identified in this manner which modulate Homer protein activity are useful for treating disorders associated with glutamate receptors such as epilepsy, glutamate toxicity, memory disorders, disorders of disorders of learning, stroke, schizophrenia, Alzheimer's disease, tissue degeneration and disorders of brain development and also for treating disorders associated with Homer protein activity which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antagonist of metabotropic glutamate receptors, or to activate an intracellular signaling pathway, especially an inositol triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 includes cardiac, muscular, vascular, neurological, psychiatric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                              Lanahan AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             when the cell is exposed to a ligand, typically an agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 1583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 /*tag= a /*tag= Homer interacting protein 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1583 BP; 344 A; 501 C; 474 G; 264 T; 0 other;
                                                                                                                                                                                                                                                                                            Leahy D, Beneken J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 64; Page 137; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Scur.
100.0%; Pred
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99US-0138493.
99US-0138494.
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                                                                                                                                                                                                                                                                                            Xiao B,
                                                                                                                          99WO-US18973.
                                                                                                                                                               98US-0097334
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                                                                                                                                                                                                                                                                                            Tu JC,
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                                                   WO200011204-A2
                                                                                                                                                                                                                                                                                                                                               P-PSDB; Y83007
                                                                                                                                                             18-AUG-1998;
09-JUN-1999;
09-JUN-1999;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 22;
                                                                                                                          18-AUG-1999;
                                                                                        02-MAR-2000
                                                                                                                                                                                                                                                                                            Worley PF,
                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor
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The present sequence encodes a human cytokine signal regulator designated CKSR-1. CKSR polypucleotides and polypeptides are useful for treating or preventing a disorder associated with increased or decreased expression or activity of cytokine signal regulators (CKSR). They are especially useful for the diagnosis, prevention and treatment of cell proliferative disorders; such as arteriosclerosis, atheroscietosis, hepatitis; cancers; such as leukemia and melanoma; and immune disorders; such as acquired immunodeficiency syndrome (AIDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps,
                                        Human; cytokine signal regulator; CKSR-1; CKSR-2; diagnosis; antiproliferative; immunomodulatory; cell proliferative disorder; arteriosclerosis; atherosclerosis; hepatitis; cancer: leukemia; melanoma; immune disorder; acquired immunodeficiency syndrome; AIDS;
             Human cytokine signal regulator CKSR-1 encoding cDNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated and purified polynucleotides encoding cytokine signal regulators for diagnosis, prevention and treatment of cell proliferative and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 21; Length 2295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 13731.
                                                                                                                                                                                                                                 "cytokine signal regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                        Corley NC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                   Location/Qualifiers
174..1604
                                                                                                      bronchitis; multiple sclerosis; ss.
                                                                                                                                                                                                                 "CKSR-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.8%; Sco
Best Local Similarity 100.0%; Pr
Matches 22; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                          98US-0189035
                                                                                                                                                                                                /product= "/note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-146886/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; Y78113
                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                           10-NOV-1998;
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Gaps

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99US-0141842.
99US-0142154.
99US-0142055.
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99US-0123180.
99US-0123788.
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99US-0128234.
99US-0128234.
99US-0128834.
99US-0130877.
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990S - 0139455
990S - 0139455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139458.
99US-0139459.
99US-0139460.
99US-0139461.
                                                      2000EP-0301439
                                                                                                                                                                                                                                                   99US-0134218.
99US-0134219.
99US-0134221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0140354
99US-0140695
99US-0140823
                                                                                                                                                                                                                                                                                         99US-01
99US-01
      Arabidopsis thallana
                      EP1033405-A2.
                                                     25-FEB-2000;
                                    06-SEP-2000.
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The polynuclectide sequences given in A26346 to A26458 encode the human secreted proteins given in Y91451 to Y91691. The human secreted proteins secreted proteins given in Y91451 to Y91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytoStatic; immunosuppressive; antiHIV; antiInflammatory; nootropic; neuroprotective; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of canoer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, athirities, infections, AlDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also used as food additives or preservatives. The proteins are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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100.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                        Duan R, Moore PA,
, Young PE, Brewer
en HS, Mucenski M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2772 polynucleotide sequence SEQ ID NO:5543.
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                                                                                                                                                                                                                                                                                                                                                                        Komatsoulis GA, Rosen CA, Ruben SM, Duan R,
Lafleur D, Wei Y, Ni J, Florence KA, Young
Soppet DR, Endress GA, Ebner R, Olsen HS, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. .v.
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                                                                                                                                                 98US-0095486.
98US-0095454.
98US-0095455.
                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                        99WO-US17130
                                                                                                                                                                                                                                                 98US-0096319
                                                                                                                       98US-0094657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8°
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-195282/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; Y91469.
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                                                              29-JUL-1999;
                                                                                                                                                    05-AUG-1998;
06-AUG-1998;
06-AUG-1998;
10-FEB-2000
                                                                                                                          30-JUL-1998
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NAMES OF COLOR COL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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100.08; Pre-
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A26364/c
ID A26364 standard; cDNA; 3070 BP
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99US-0162142
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                                                                                                                                                    99US-0155
99US-0155
99US-0156
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Matches 21; Conserv
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Query Match

ò g A26364;

6-0CT-1

-OCT-1

-0CT-

OCT-1

-0CI

3-0CT-

39-SEP-

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represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiporiatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiparkinsonian; nootropic; antidabetic; hypotensive; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; cardiant; thrombolytic; captulant; vasotropic; antidabetic; hypotensive; cardiant; antifungal, antithromatic; antithyroid; antibacterial; antiviral; antimunosuppressive; antioning the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative cused to treat cancers, proliferative disorders, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, candiovascular disease, storme, when the proteins and mucleic acids may be stormed, systemic lupus erythematosus, severe combined immunodeficiency corrections.
                                                                                        Immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; arative disorder; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; collesterol disease; diabetes mellitus; hypothyroidiam; collesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; bone damage; cartilage damage; antiinflammatory disease; coaquiation; thrombosis; contraceptive; ss.
                                           vulnerary, antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                          Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhance coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 4726-4728; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
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P-PSDB; B43008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200058473-A2
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-CT-2000
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/*tag= b /note= "given in the specification as SEQ ID NO: 119 and specifically claimed in claim 4"

/*tag= c 225..1190 /*tag= d

sig_peptide mat_peptide WO200037634-A2

99WO-US29854 98US-0112837 98US-0113485 99US-0113485

17-DEC-1999;

29-JUN-2000

18-DEC-1998; 21-DEC-1998; 16-DEC-1999; (CURA-) CURAGEN CORP

WPI; 2000-442664/38.

Shimkets RA;

P-PSDB; B14313.

/*tag= a /product= "SECX polypeptide" /transl_except= (pos:999..1001,aa:Xaa) /transl_except= (pos:1170..1172,aa:Xaa) /note= "Xaa= unknown"

misc_feature

Human; secreted protein; SECX; cancer; cytostatic; vaccine; ss.

Location/Qualifiers

Homo sapiens

174..1193

Key

Human secreted protein cDNA clone 3903091.

21-NOV-2000 (first entry)

A62524;

A62524 standard; cDNA; 1201 BP

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RESULT 1 A62524/c

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Claim 5; Page 118-120; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                               (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
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The present sequence is one of 23 nucleic acids, collectively referred to as SECX nucleic acids, which encode novel secreted human proteins. Various SECX nucleic acids were cloned into insect cells and human embryonic kidney 293 cells and quantitative expression of the clones was analysed. By detecting the presence of a SECX nucleic acid or polypeptide in a sample it is possible to diagnose a pathological condition, especially cancer, associated with aberrant SECX expression or activity. Antibodies, and primers and probes are used, respectively, to detect SECX polypeptides and sECX nucleic acids in this method.
SECX nucleic acids, polypeptides and antibodies are also useful for treating, preventing or delaying conditions associated with aberrant SECX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Best Local Similarity
Matches 20; Conserv
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Gaps

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0.8%; Score.21; DB 21; Length 4021; 100.0%; Pred. No. 3.7; tive 0; Mismatches 0; Indels (

Query Match 0.8 Best Local Similarity 100. Matches 21; Conservative

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New SECX polypeptide useful for diagnosing, treating and delaying pathological conditions, especially cancer

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A99466;

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codes for DNA polymerase delta (W03132), an enzyme which has 3'-5' exonuclease activity. Mutations of the gene lead to a replication error phenotype (RBR+) in some colorectal cancers. Wariants at codon 502 (proximal to the ExoIII domain) and codon 506 (within ExoIII) of the gene were separately found in 2 colorectal cancer non-polyposis colorectal cancer, owing to a mutation in a pol delta allele, can be treated by administration of the gene. Patients with RBR+ tumours can be treated to prevent accumulation of somatic mutations leading to resistance to cytostatic agents. The gene can also be used to diagnose a predisposition to colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA polymerase delta mutant and corresp. coding sequence - associated with replication error phenotype in colorectal tumours, useful for diagnosis and therapy
                                ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A cDNA clone (T35869) corresponding to the human pol delta gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakuranetin synthetase; naringenin 7-0-methyltransferase; NOMT; antibacterial; transgenic plant; ds.
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              DNA polymerase delta; pol delta; colorectal tumour; cancer; gene therapy; diagnosis; replication error; RER+; DNA repair;
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11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 13-17; 32pp; English.
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100.08; Pic
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ID A99469 standard; DNA; 4371 BP
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                                                                                                                                                                                                                                                                                                                                              Vogelstein B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.8 Best Local Similarity 100. Matches 20; Conservative
                                                                                                                                      /*tag=
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                                                                  Homo sapiens
                                                                                                                                                                      WO9621026-A1
                                                                                                                                                                                                                                        02-JAN-1996;
                                                                                                                                                                                                                                                                                                                                              Kinzler KW,
                                                                                                                                                                                                                                                                         30-DEC-1994;
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                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector. The sakurānetin synthetase protein has antibacterial activity and is used to produce transgenic plants with antibacterial characteristics. The present sequence represents genomic DNA encoding the enzyme of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a sakuranetin synthetase gene encoding a protein with naringenin 7-0-methyltransferase (NOMT) activity and promoter activity. The invention includes a recombinant vector including the sakuranetin synthetase DNA and host cells transformed with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sakuranetin synthetase gene encoding protein with naringenin 7-0-methyltransferase activity in rice cells and promoter activity, used to derive sakuranetin from naringenin easily in plants to impart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                       Sakuranetin synthetase; naringenin 7-0-methyltransferase; NOMT; antibacterial; transgenic plant; ds.
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 36-37; 57pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08; PE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial characteristics -
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            BP.
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                                                                                                               A99466/c
ID A99466 standard; DNA; 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-1996 (first entry)
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                        Sakuranetin synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                           WO200052174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; B26843.
                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1999;
                                                                                                                                                                                                      26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
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Query Match

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EX PX PX PX

14

RESULT 1 T35869/c

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This invention relates to a sakuranetin synthetase gene encoding a protein with naringenin 7-0-methyltransferase (NOMT) activity and promoter activity. The invention includes a recombinant vector including the sakuranetin synthetase DNA and host cells transformed with the vector. The sakuranetin synthetase protein has antibacterial activity and is used to produce transgenic plants with antibacterial characteristics. The present sequence represents the sakuranetin synthetase gene of the
                                                                                                                                                                                                                     Sakuranetin synthetase gene encoding protein with naringenin 7-0-methyltransferase activity in rice cells and promoter activity, used to derive sakuranetin from naringenin easily in plants to impart antibacterial characteristics -
                                                                                                                                                                                                                                                                                                                   Example 3; Page 33-36; 57pp; Japanese.
                                                                                                            (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                    03-MAR-2000; 2000WO-JP01306.
                                                                        99JP-0057748
                                                                                                                                                                                     WPI; 2000-572186/53.
                                                                        04-MAR-1999;
08-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                Kodama O;
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.; O Length 4371; .0; Indels 0.8%; Score 20; DB 21; 100.0%; Pred. No. 11; tive 0; Mismatches .0, 2007 tgttttgctttctttcctt 2026 1227 TGTTTTGCTTTCCTT 1208 Query Match 0.8 Best Local Similarity 100. Matches 20; Conservative ò q

Sequence 4371 BP; 1281 A; 1008 C; 949 G; 1133 T; 0 other;

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Gaps

Search completed: June 20, 2001, 23:25:27 Job time: 13424 sec

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09382086
Fatent No. 6201106
GENERAL INFORMATION
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Budghn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/189,035
HARIER FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                     APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guaghn, Maral J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/189,035
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEO ID NOS: 6
SOFTWARE: PERL PROGRAM
US-08-759-038-11
US-08-758-314-11
US-08-471-0668-30
US-08-471-0668-30
US-08-48-956-30
US-08-599-491-30
US-08-757-653-30
US-08-756-386-30
US-08-756-386-30
US-08-759-038-30
US-08-759-038-30
US-08-759-038-30
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US-08-759-038-30
US-08-759-038-30
US-08-758-12
US-08-471-0668-12
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Pred. No. 0.34;
0; Mismatches
                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1526
                                                                                                                                                                                                                                           ; Sequence 3, Application US/09189035; Patent No. 6020165; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE: -
; OTHER INFORMATION: 2280326
US-09-189-035-3
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
Best Local 22; Conservative
  ORGANISM: Homo sapiens
    SEQ ID NO 3
LENGTH: 2295
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-09-382-086-3
                                                                                                                                                                                                                                   JS-09-189-035-3
   TYPE: DNA
   00000000000
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                                                                              (without alignments)
5433.006 Million cell updates/sec
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1 cttctcttgcacttgcggat.....aatggttcattttaaaagtt
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                                                                   89.51 Seconds
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                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                    time
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US-08-682-853A-11
                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-254-359A-11
                                                                   June 20, 2001, 19:27:34; Search
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US-08-481-238-11
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                                                                                                                                                                          317530 segs, 92630169 residues
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                                                 - nucleic search, using sw model
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                                                                                                                                             OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
                                                                                                        US-09-425-501-1
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Match
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                                                                                                                  score:
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Maximum DB
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Perfect
                                                                    Run on:
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No.
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1651 tgcctccatctcctccatca 1670
                                                180 TGCCTCCATCTCCTCCATCA 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.84
Best Local Similarity 100.(
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                    STREET: 1001 G St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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MOLECULE TYPE: CD
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PCT-US96-00005-1
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US-08-718-905-1
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APPLICANT: Kinzler, Kenneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION BRRORS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street N.W.
                                                                                                                                                                                                   Length 2295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 20; DB 1; Length 3435; 100.0%; Pred. No. 3.2; 0; Mismatches 0; Indels

    Indels.

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COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTED:
CLASSIFICATION NUMBER: US/08/366,577
FILING DATE: 12-DEC-1994
CLASSIFICATION: SATAB A.
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.48554
TELEFHONE: 202-508-9100
TELEFA: 202-508-9100
TELEFA: 202-508-9100
TELEFA: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARRATERISTICS:
LENGTH: 3435 base pairs
TYPE: MORIFACE COUNTY
MORIFACE CHARRATERISTICS:
CANNEDDINES: Gouble
                                                                                                                                                                                             Query Match 0.8%; Score 22; DB 4; Best Local Similarity 100.0%; Pred. No. 0.34; Matches 22; Conservative 0; Mismatches
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; Sequence 1, Application US/08366577
; Patent No. 5728523
                                                                                    FEATURE: -
CTHER INFORMATION: 2280326
US-09-382-086-3
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.8
Best Local Similarity 100.
Matches 20; Conservative
                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1001 G Str
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
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MOLECULE TYPE: CDNA
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US-08-366-577-1
SEQ ID NO 3
LENGTH: 2295
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Patent No. 6063756
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Donovan, Judith C.
APPLICANT: Slaney, Annette C.
APPLICANT: Slaney, Annette C.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET33 AND CRYET34
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                                                                                               APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Renneth W.
TITLE OF INVENTION: POLYMERASE DELTA MUTATIONS IN COLORECTAL
TITLE OF INVENTION: TUMORS WITH REPLICATION ERRORS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3435
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00005
FILING DATE: 2-JAN-96
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 3.7 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.53505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                              ADDRESSEE: Banner & Allegretti, Ltd STREET: 1001 G Street N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
RESULT 4
PCT-US96-00005-1/c
PCT-US96-00005-1/c
; Sequence 1, Application PC/TUS9600005
; GENERAL INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1257; 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Francis Barany et al
TITLE OF INVENTION: Thermostable Ligase Mediated DNA
TITLE OF INVENTION: Amplification System For The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: George M. Yahwak
REGISTATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-933/CIT-2047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 9.7 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/971,095
FILING DATE: No. 5494810ember 2nd 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: MACIOSOft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,785
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticutt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08343785
Patent No. 5494810
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Sc
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1073 accacctccacctccacca 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           921 accacctccacctccacca 939
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: THE TITLE OF INVENTION: AM NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (509)..(1088)
US-09-230-222-2
                            mat_peptide
(181)..(1088)
                                                                                                                                                                                                                     LOCATION: (453)..(508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                          CDS (181)..(452)
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                                                                                                                                                                                           NAME/KEY: intron
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                                                      COCATION:
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| Sequence 2, Application US/0923022A
| Patent No. 6159720
| GENERAL INFORMATION:
| APPLICANT: HAMYA, TONU
| APPLICANT: HAMYA, TONU
| APPLICANT: HAMYA, TONU
| APPLICANT: HAMYA, TONU
| APPLICANT: SUMIDA, NAOMI
| APPLICANT: SUMIDA, NAOMI
| APPLICANT: MORAKAMI, TAKESHI
| APPLICANT: MONO, TOSHIAKI
| TITLE OF INVENTION: CONTAINING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.7%; Score 19; DB 3; Length 807, 100.0%; Pred. No. 9.5;
COMPOSITIONS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/718,905 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOBI:003
TELECOMMUNICATION INFORMATION:
TELECHORE: (512) 418-3000
                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2598 atttaataaatggttcatt 2616
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                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single
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LOCATION: (118)..(180)
FEATURE:
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LOCATION: (118)..(180)
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Matches 19; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-718-905-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                 Texas
                                                                                                                                                           STATE: Texa COUNTRY: Un ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 1257
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APPLICANT: Zebala, John
APPLICANT: Nickerson, Deborah
APPLICANT: Nickerson, Deborah
APPLICANT: Kaiser, Jr., Robert J.
APPLICANT: Hood, Leroy
TITLE OF INVENTION: A THERMOSTABLE LIGASE MEDIATED DNA
TITLE OF INVENTION: AMPLIFICATION SYSTEM FOR THE DETECTION OF GENETIC. DISEASES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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APPLICANT: Francis Barany et al
TITLE OF INVENTION: Thermostable Ligase Mediated DNA
TITLE OF INVENTION: Amplification System For The
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 19; DB 3;
100.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                              ADDRESSEE: Nixon Peabody LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-UN-1995
APPLICATION NUMBER: US 08/343,785
FILING DATE: 22-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/971,095
FILING DATE: 02-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,447
FILING DATE: 03-MAY-1990
ATTORNEY/AGENT INFORMATION:
ANDER CALLAND AND AND ATTORNEY/AGENT INFORMATION:
AND ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/267
TELEPHONE: 716-263-1304
TELEFRAX: 716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,458
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Yahwak & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08343785
; Patent No. 5494810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%; SC
Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-946-458-7
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                           Barany, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2051 base.pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                           CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                              COUNTRY: U ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-343-785-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                DISEASES
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                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A THERMOSTABLE LIGASE MEDIATED DNA TITLE OF INVENTION: AMPLIFICATION SYSTEM FOR THE DETECTION OF GENETIC NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,221

FILING DATE: US/08/1995

PRIOR APPLICATION 1995

PRIOR APPLICATION NUMBER: US/08/343,785

FILING DATE: 22-NOV-1994

PRIOR APPLICATION NUMBER: US 08/343,785

FILING DATE: 22-NOV-1994

PRIOR APPLICATION NUMBER: US 07/971,095

FILING DATE: 02-NOV-1992

PRIOR APPLICATION NUMBER: US 07/518,447

FILING DATE: 03-NAY-1990

ATTONNEY/AGENT INFORMATION:

NAME: GOLDMAN NUMBER: US 07/518,447

FILING DATE: 03-NAY-1990

ATTONNEY/AGENT INFORMATION:

NAME: GOLDMAN NUMBER: US 07/518

REGISTENENCE/DOCKET NUMBER: 19603/267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
CITY: Rochester STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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100.0%; Pred. No.
Live 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           APPLICANT: Nickerson, Deborah
APPLICANT: Kaiser, Jr., Robert J.
APPLICANT: Hood, Leroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08946458
Patent No. 6054564
                                                                                                                                                                    Sequence 7, Application US/08462221
Patent No. 5830711
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: 716-263-1304
1210 etececeacetectecace 1228
                         1665 CTCCCCCACCTCCTCCACC 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1210 ctccccacctcctccacc 1228
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SEQUENCE CHARACTERISTICS:
LENGTH: 2051 base pairs
                                                                                                                                                                                                                                           APPLICANT: Barany, Francis
APPLICANT: Zebala, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-462-221-7
                                                                                                                                                US-08-462-221-7/C
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DETECTION OF GENETIC DISEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Barany, Francis
APPLICANT: Sebala, John
APPLICANT: Nickerson, Deborah
APPLICANT: Maiser, Jr., Robert J.
APPLICANT: Hood, Leroy
APPLICANT: Hood, Leroy
TITLE OF INVENTION: A THERMOSTABLE LIGASE MEDIATEI
TITLE OF INVENTION: AMPLIFICATION SYSTEM FOR THE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: OFC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9.7
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Nixon Peabody LLP
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,221
FILING DATE: 05-UNN-1995
APPLICATION NUMBER: US 08/343,785
APPLICATION NUMBER: US 08/343,785
APPLICATION NUMBER: US 08/343,785
                                 PRIOR DATE: 22-07-1234
PRIOR DATE: 22-07-1234
APPLICATION NUMBER: US 07/971,095
FILING DATE: 02-007-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,447
FILING DATE: 03-MAY-1990
ATTOMNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERNICE/DOCKET NUMBER: 19603/267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICAL.
FILING DATE: 22-NOV ...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,095
APPLICATION NUMBER: 02-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/518,447
MBER: US 08/343,785
22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08946458 Patent No. 6054564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1210 ctcccccacctcctccacc 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 1725 CTCCCCACCTCCTCCACC 1707
                                                                                                                                                                                                                                                                                               TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
EUGTH: 2111 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.79
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon Pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: CLIMATERY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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APPLICANT: Kaiser, Jr., Robert J.
APPLICANT: Hood, Leroy
TITLE OF INVENTION: A THERMOSTABLE LIGASE MEDIATED DNA
TITLE OF INVENTION: A MPLIFICATION SYSTEM FOR THE DETECTION OF GENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,221
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/971,095
FILING DATE: NO. 5494810ember 2nd 1992
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-933/CIT-2047
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.7%; Score 19;
                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Prv
0;
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; Sequence 1, Application US/08462221
; Patent No. 5830711
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APPLICANT: Zebala, John
                                                                                                                         COMPUTER: floppy disk
: 25 Skytop Drive
Trumbull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2111 base pairs
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Best Local Similarity 100.0
Matches 19; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 14603
COMPUTER READABLE FORM:
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                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                         Connecticutt
USA
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: U.S.A.
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
US-08-343-785-1
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                                                             COUNTRY: U
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Length 24; Indels

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                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
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APPLICANT: MASUCCI, MATIA G.
APPLICANT: MASUCCI, MATIA G.
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 19;
100.0%; Pred. No.
                                                                                           30,727
19603/267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Financial Center CITY: Boston
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Patent No. 5833991
                                                       NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REPERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
TELEFAN: 716-263-1304
TELEFAX: 716-263-1304
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2111 base pairs
TYRE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1210 ctccccacctcctccacc 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1725 CTCCCCCACCTCCTCCACC 1707
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03-MAY-1990
                                    ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%
Best Local Similarity 100.C
Matches 19; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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STATE: MA
COUNTRY: USA
TO: 02111
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; MOLECULE TYPE:
US-08-946-458-1
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US-08-529-190B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Lycopersicon esculentum cv 'Rutgers Large ORGANISM: Red'
                                                                APPLICANT: MCK. BIRD, David
APPLICANT: WILSON, Mark A.
TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATION
OPERATION
OPERATION
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/248,474
FILING DATE: 25-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 3207E-535
TELECOMMULCATION INFORMATION:
TELEPHONE: (415) 542-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 1..131
; OTHER INFORMATION: /standard_name= "DB# 275'
US-08-248-474-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.7%; Score 18; DB 1;
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Sequence 102, Application US/08248474; Patent No. 5612471; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-756 849-102/c
;.Sequence 102, Application US/08756849
; Patent No. 6093810
                                                                                                                                                                                                                                                            2IP: US
2IP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%; Soc
Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1305 ccacctccacctccagcc 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 CCACCTCCACCTCCAGCC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                    STREET: Steuart Stre
CITY: San Francisco
STATE: California
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APPLICANT Bird, David McK.
APPLICANT Wilson, Mark A.
TITLE OF INVENTION: Mear A.
TOTAL CORPORESSE:
ADDRESSE: Townsend and Townsend and Crew LLP
CORPORE SERVE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: San Francisco
COMPUTE: California

ZIP: 94111-3834

COMPUTE: Right Pool Compatible
OCHAPHY: IBM PC CONS/MS-DOS
SOFTWARE: Patentin Release #10. Version #1.30.
OCHAPHY: Patentin US/08/756,849
FILING DATE: 25-MV-1996
CLASSIFCATION NUMBER: US/08/756,849
FILING DATE: 25-MV-1996
CLASSIFCATION NUMBER: US/08/756,849
FILING DATE: 25-MV-1996
CLASSIFCATION NUMBER: 023070-053510US
FILING DATE: 25-MV-1996
CLASSIFCATION NUMBER: 023070-053510US
FILING DATE: 25-MV-1994
FILING DATE: 35-MV-1994
FILING DATE: 30-MV-1994
FILING DATE: 30
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Query Match 0.7%; Score 18; DB 3; Length 131; Best Local Similarity 100.0%; Pred. No. 28; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

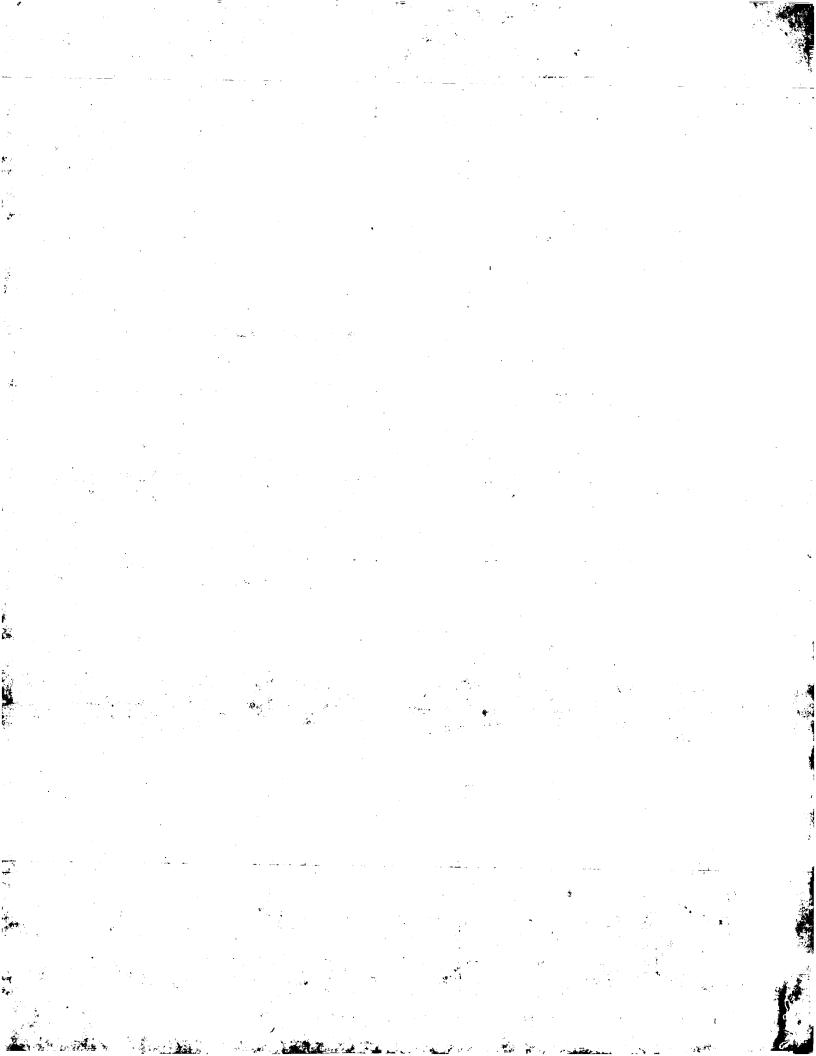
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1305 ccactccactccagcc 1322

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105 CCACCTCCACCTCCAGCC 88

Search completed: June 20, 2001, 23:22:20 Job time: 14086 sec



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em_esthum27: em_esthum28:

em_estin4: em_estom1:

em_estom2 em_estov1 em_estov2

em_estin2

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em_esthum25 em_esthum26

em_esthum17: em_esthum18:

em_esthum14: em_esthum15: em_esthum13

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June 20, 2001, 17:22:49; Search time 1942.94 Seconds (without alignments) 12771.234 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                          OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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em_esthum9:
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gb_est36:*
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Perfect score:
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em_estpl10:

em_estro] em_estro

estro4

em_estro2

em_estpl6: em_estpl7:

em_estp18

em_estpl9

em_estpl2: em_estpl3:

em_estpl]

em_estp14 em_estpl5 em_estro20:*
gb_est25:*
gb_est26:*
gb_est27:*
gb_est28:*
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gb_est30: gb_est31: gb_est32: gb_est41: gb_est42: gb_est42: gb_est44:

gb_est46: gb_est47:

em_estro19:*

em_estro14:

em_estro10

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em_estro16 em_estro17: em_estro18:

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gb_est98:*
em_esthum29:*
em_esthum30:*
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em_esthum32:
em_esthum33:
em_estom3:*
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9b_est49:*
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9b_est66:*
9b_est60:*
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em_gss_vrt3:* gb_gss1:* gb_gss2:* gb_gss3:* gb_gss4:* gb_gss6:*

9b_9ss6:*
9b_9ss7:*
9b_9ss8:*
9b_9ss9:*
9b_9ss10:
9b_9ss10:
9b_9ss11:

gb_gss13: gb_gss14: gb_gss15:

em_gss_other:

em_gss_hum8:

em_gss_hum9

hum7

em_gss_invl em_gss_inv2 em_gss_inv3

em_gss_hum5

em_gss_pln1:'em_gss_pln2:' em_gss_rod1:

em_gss_pro:

em_gss_rod2: em_gss_rod3:

em_gss_rod5: em_gss_vrt1:

em_gss_fun:* em_gss_huml:*

em_gss_hum2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_gss28: gb_gss29:

gb_gss30

gb_gss22: gb_gss23: gb_gss24: gb_gss25: gb_gss26: gb_gss27:

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gb_gss31: gb_gss32:

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	Description	AL526626 AL526626	EST37544				AU142666 AU142666	- 3	BE148072 RC3-HT023			BE731111 601566327	N95702 yy60c07.rl	7940910	AW673234 ba64c12.x		AL079676 DKFZp434B	BG390996 602417681	BG391003 602417689	60241//6		AA885055 aml1c01.s	AI929146 au65f06.y	BG426480 602492882	R56489 y994a01.rl	BGI68604 602344810 H18215 vn47h11 s1	AW590436 hq44h10.x	AA846712 aj41c05.s	AW956469 EST368539	AI306688 qw25b09.x	D3/242 HUM28/BUSB	A1341434 GX31110.X A1910678 ++37h04 v	H06129 v177h09 r1	BE787088 601476633	BE019589 ba84b08.v	Ξ	M79145 EST01293 Su	ni30d03	N63410 yy60C07.s1	one t tit
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SUMMARIES	QI	AL526626	AW963370	AW379048	AW071606	AI928895	AU142666	AI650710	BE148072	AW664122	AU159926	BE731111	N95702	AI750422	AW673234	BG111973	AL079676	BG390996	BG391003	AW451579	AI061122	AA885055	AI929146	BG426480	R56489	BG1686U4	AW590436	AA846712.	AW956469	AI306688	D3/242	A1341434 A1910678	H06129	BE787088	BE019589	F12990	M79145	AA515859	N63410	
	- :	105	122	115	111	103	154	23	164	119	108	139	18/	24	119	173	105	153	153	116	15	13	103	153	187	157	118	12	122	18	0 1	103	157	140	162	157	59	8	136	1
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de	Query Match	22.3	20.7	20.6	18.0	18.7	17.8	17.5	16.5	16.4	15.2	15.2	2. 4. 2. a	14.7	14.6	14.5	14.4	13.3	13.3	13.2	12.8	12.8	12.5	12.5	12.2	12.0	11.8	11.6	11.5	11.0	9 5	10.4	10.2	10.0	9.7	9.7	7.6	9.0	9 0	
	Score	585	543	541	496	479	467	460	432	430	398	398	39T	387	383	381	379	349	349	347	335	335	329	327	320	314	311	304	301	289	6/2	272	267	262	255	254	254	253	202	† 1
	Result No.	7	ım		o o		- α	υ 0	Н	c 11	c 12	FT -		c 16		18	19	20	21		c 24		56	27	28	30	c 31			0 34		32		39	40	41	4	4 4	י ני קייני	•

ALIGNMENTS

AL52666 AL52626 B51 bp mRNA EST 13-FEB-2001
LOCUS
DEFINITION AL526626 LTI_NFL003_NBC3 Homo sapiens CDNA clone CSODC020YO18 5
ACCESSION AL526626.

AL526626 LTI_NFL003_NBC3 Homo sapiens CDNA clone CSODC020YO18 5
ACCESSION AL526626.

AL526626 G1:12790119
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
ORGANISM Homo sapiens
ELARIYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Pull-length CDNA libraries and normalization
JOHRNAL Unpublished (2001)
COMMENT COLTACT: Genoscope

/tissue_type="neuroblastoma cells"
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a Not!-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: filang@lifetech.com URL:
http://fullength.invitrogen.com"
4 others ö 2019 2079 2139 2199 2259 1780 aagtagaagagcagcgtgaacaggaagctaagcatgaacgcattgaaaacgatgttgcca 1839 61 AAGTAGAAGAGCAGCGTGAACAGGAAGCTAAGCATGAACGCATTGAAAACGATGTTGCCA 120 300 420 2320 tttaaaagaagaagaacactgccttgattatacgaatacactcagaaagtacatttagcttg 2379 9 Gaps Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. 2140 aatttggtcaaataaaccactaagtattaagcatggacagctgttgttagagtagcagat 2260 gaaattgaaatcttgagggcagctgtatctactaatgagccttattccatttcctgatgt 541 GAAATTGAAATCTTGAGGGCAGCTGTATCTACTAATGAGCCTTATTCCATTTCCTGATGT ö Query Match 22.3%; Score 585; DB 105; Length 851; Best Local Similarity 99.7%; Pred. No. 1.6e-301; Matches 685; Conservative 0; Mismatches 2; Indels 0 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cS0Dc020Y018"
/clone_lib="LTI_NFL003_NBC3"
/sex="male" Location/Qualifiers 263 source BASE COUNT ORIGIN 2020 FEATURES g qq qq Qγ Dρ Ω Op ōλ g ò q ò ò δ ŏ 염 ò δ

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human.
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/clone_lib="NIH_MGC_93"
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/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                       Homo sapiens
Bukaryotas; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 652)
1 (hases 1 to 652)
Nath-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC
                                                                                                             BG288785 652 bp mRNA EST 21-FEB-2001 602388115F1 NIH_MGC_93 Homo sapiens CDNA clone IMAGE:4517163 5'
                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
http://maqe.llnl.gov
Plate: LLAM10409 row: m column: 04
High quality sequence stop: 638.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    709 atttetttgatetatggaaagaaaaaatgttgeaagatacagaggataagaggaaggaaa 768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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2380 tagtgttgaattctcttaaaggaatgc 2406
                  661 TAGTGTTGAATTCTCTTAAAGGAATGC 687
                                                                                                                                                                          BG288785.1 GI:13043972
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AUTHORS
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EST375443 MAGE resequences, MAGH Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
                                                                                                                           TGTCTTTGCAAGATATAACAATGAGGAAAGCTTTCCGAAGTTCTACAATTCAAGACCAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaspard, R., Gay, C.,
               aaacaagacctcagacatacgtggatcatatggatggatcttactcactttctgccttgc
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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
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100.0%; Pred. No. 5e-279;
Live 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, M
/note="Vector: pBluescriptSKm"
125 c 140 g 164 t ·
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Mammalia; Eutheria; Primates;
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AW963370.1 GI:8153206
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Plate: 187
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AW071606
AW071606.1 GI:6026604
                                                                                                        Matches 541; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dcone_lib="Hr0220"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: puc18; Site_1: 
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This equence was derived from the following URL
(http://www.luduig.org.br/scripts/gethtml2.pl?tl=RC3*L2=RC3-HT0230-
201199-013-c11&t3=1999-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 712.
Location/Qualifiers
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RC3-HT0230-201199-013-c11 HT0230 Homo sapiens CDNA, mRNA sequence.
AW379048
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 718)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
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Fax: +55-11-2707001
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Itssue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW071606 497 bp mRNA EST 09-MAR-2000 wt94a11.x1 NCI_CGAP_GGG Homo sapiens cDNA clone IMAGE:2515100 3'
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          DB 115; · Length 718;
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                              Pred. No. 5.9e-278;
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20.6%; Scott 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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FEATURES

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Bases I to 540,
Hillier, L., Allen, M.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Morre, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., Washt-NCI human EST Project
Unpublished (1907)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: brain; Vector: pBluescript SK (Stratagene); Ste_1: SStL; Site_2: Xho!; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE.Consortium (info@image.llnl.gov) for further information.
Seg primer: -40UP from Gibco
High quality sequence stop: 479.
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                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2519651"
/clone_lib="Schneider fetal brain 00004"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
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Pred. No. 9.2e-245;
0; Mismatches 1;
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76 q 173 t
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99.8%;
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Contact: Wilson RK
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Fax: 314 286 1810
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Clone distribution: NCI-CGAP clone distribution information can
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          found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 746 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                     /tissue_type="pooled germ cell tumors" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.9%; Score 496; DB 111;
100.0%; Pred. No. 7.2e-254;
ive 0; Mismatches 0;
                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_GC6"
                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2515100"
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Best Local Similarity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
Ota,T., Nishikaa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                             2515
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                                                                                                                                                9
                                                                                                                                                                                                                                                   AU142666 779AA1 Homo sapiens CDNA clone Y79AA1000685 5', mRNA
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Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
11532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 17.8%; Score 467; DB 108; Best Local Similarity 100.0%; Pred. No. 2.5e-238; Matches 467; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="retinoblastoma"
/cell_line="Y79"
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183 c 141 g 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Y79AA1000685"
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AU142666
AU142666.1 GI:11004187
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HRI human cDNA project
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/organism="Homo sapiens"
/dp_xref="taxon:9666"
/db_xref="taxon:9666"
/clone='IRAGE:465531"
/clone='IRAGE:46553
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1444 row: j column: 24
High quality sequence stop: 726.
                                                                                                                                                                                                                                                                                     409
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602258493F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4655351
mRNA sequence.
BG492540
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/db_xref="taxon:9606"
/clone="lMAGE:2306746"
/clone=llb="NCI_CGAP_GG6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                  /organism="Homo sapiens"
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BE148072.1 GI:8610796
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 971 Std Error: 0.00
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Email: cgapbs -r@mail.nih.gov
Emsil: cgapbs -r@mail.nih.gov
Itssue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI650710 462 bp mRNA EST 17-DEC-1999 wb259006.xl NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2306746 3',
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                                                                                                                       1690 agccaaagcgccatccatcaaccctacctgtaatcagtgatgccaggagtgtgctactgg 1749
                                                                                                                                                                                                                                                                                                                                                                  gcattgataaatattacaaaactgaatgcaaatgtcctttgtggtgcttgttccttgaaa 1989
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 46)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (
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                                                           Length 821;
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                                                             DB 154;
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Seq primer: -400P from Gibco
High quality sequence stop: 438.
Location/Qualifiers
    5
   153
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Unpublished (1997)
                                                                                           Matches 461; Conservative
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A1650710
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                                                                           Similarity
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   247
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TITLE
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COMMENT

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/note="Vector::PT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 147592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Mataukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2405
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Pred. No. 1.4e-234;
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Matches 430; Conservative
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AW664122/C
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                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                             Length 555;
                                (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                            16.5%; Score 432; DB 164;
99.8%; Pred. No. 1.4e-219;
live 0; Mismatches 1;
                               U.S.A. 97
                                                Contact: Simpson A.J.G.
                         sequence tags
Proc. Natl. Acad. Sci.
20202663
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        Simpson, A.J.
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                 Brazil
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
EST 06-APR-2000 sapiens cDNA clone IMAGE:2971330 3',
                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life machinologies.
                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIIonal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="2 pooled high-grade transitional cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: polyT not found Seq primer: -40Up from Gibco High quality sequence stop: 394. Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2971330"
                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
  mRNA
Homo
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  AW664122 430 bp
hi04e06.xl NCI_CGAP_GU1
                                              mRNA sequence.
AW664122
AW664122.1 GI:7456662
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Homo sapiens
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HRI human cDNA project (Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department'of
Virology, Institute of Medical Science, University of Tokyo, and
                                                      2496 gatatgattttgcttgcctataggagttaaaaacttttccatgtgaaatactctgactta 2555
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                                                                                                                                                                                                                                                                           AU159926 565 bp mRNA EST 25-OCT-2000
AU159926 Y79AA1 Homo sapiens CDNA clone Y79AA1000685 3', mRNA
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1532-3 Yana Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="retinoblastoma"/cell_line="Y79"
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87 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Y79AA1000685"
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Genomics Laboratory
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="INAGE:3841135"
/clone_lib="NHI-MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="BHIOB (phage-resistant)"
/lab_host="BHIOB (phage-resistant)"
/note="Organ: placenta; Vector: pOTB): Site_l: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhoI sites using the
following 5' adaptor: GGCAGGGGO. Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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E 1 (bases 1 to 727)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM532 row: e column: 08 High quality sequence stop: 669.

Location/Qualifiers

1.727
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214 ggtgaactggcacaaaggttaatctcaagatgccgctagtgaaaagaaacatcgatccta 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE731111 727 bp mRNA EST 15-SEP-2000 601566327F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841135
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1larity 99.8%; Pred. No. 2.3e-201;
Conservative 0; Mismatches 1;
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Kifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlfing, P., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pr7735 (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not 1; Site_2: Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens .
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET
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sapiens cDNA
                                                                                                                                                                                                                        GGTGAACTGGCACAAAGGTTAATCTCAAGATGCCGCTAGTGAAAAGAAACATCGATCCTA
                                                 atatttccttggcaaatataattagacaactaagtagcctaagtaaatatgctgaagata
                                                                                                              tatttggagaattattcaatgaagcacatagtttttccttcagagtcaactcattgcaag
                                                                                                                                                                            ttttcgatcgcaagactttgcctattccattacagagacgtacgatgtttgtgaacagc
                                                                                                                                                                                                                                                                                                                                                                                    517 TTTTCGATCGCAAGACTTTGCCTATTCCATTACAGGAGACGTACGATGTTTGTGAACAGC
                                 ggcacttgtgccacacagcactgcctagaggcattaagaatgaactggaatgtgtaacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:277932"
/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N95702 443 bp mRNA EST
YY60c07.rl Soares_multiple_sclerosis_2NbHMSP Homo
clone IMAGE:277932 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:3896308"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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JOURNAL
COMMENT
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AUTHORS
                               274
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KEYWORDS
SOURCE
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N95702
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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                                                                                                                                                                                                sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. Fatima Bonaldo
                                                                                                                                       (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple scherosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NIDS/AUH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1223407 481 bp mRNA EST 29-NOV-1998
424840.X1 Soares_testis_NHT Homo sapiens cDNA clone IMACE:1838466
3' similar to SW:Y569_HUMAN 092558 HYPOTHETICAL PROLINE-RICH
PROTEIN KIAA0269:;, mRNA sequence.
                                                                     double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 481)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2142
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strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2143 ttggtcaaataaaccactaagtattaagcatggacagctgttgttagagtagcagattca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GTCCTTTGTGGGGGCTTGTTCCTTGAAAATGTTTGGTCATTCTAGTGTTTTGCTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 CCTTATAATAAATGACCCTTTTCCTCCATAACTTTTGATTTCTAAGGAAAATATTAGCAT
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                                                                                                                                                                                                                                                                                                                                                                      Length 443;
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                                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 391; DB 187;
100.0%; Pred. No. 1.2e-197;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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AI223407.1 GI:3805610
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                                                                                                                                                                                                                                                                                     1636 cccatgttccattaatgcctccatccctccatcacaagttatacctgcttctgagccaa 1695
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                    Length 481;
                                                                                                                                                                                                                                                                      1; Indels
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 719 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 326.
Location/Qualifiers
                                                                                                                                                                                                                                                 Score 389; DB 17;
Pred. No. 1.4e-196;
0; Mismatches 1;
                                                                                  /clone="IMAGE:1838466"
/clone_11b="Soares_testis_NHT"
/lab_host="DH108"
                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 20, 2001, 22:22:15
Job time: 17966 sec
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                                                                                                                                                                                                                                                  14.8%;
99.8%;
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Best Local Similarity 99.8
Matches 439; Conservative
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Plasmid pCisEBON f
Nucleotide sequenc
DNA clone pCEK CI.
Human secreted pro
FLGA insert stabil
Genomic clone GilF
Genomic DNA encodi Epstein Barr Virus
Gene encoding Plas
Kaposi's sarcoma-a
KSHV LUR DNA (nicl
KSHV LUR DNA (nicl
KSHV LUR DNA (nicl
KSHY long unique c
Human secreted pro

Partial mouse WRN
Nephila clavipes s
N.Clavipes draglin
Nephila clavipes s
N. Clavipes spider
Arabidopsis thalia
Brush-1 cDNA Probe
Brush-1 cDNA Probe
Brush-1 cDNA Probe
Brush-1 cDNA Probe
Brush-1 cDNA CONE
New DNA sequence i
New DNA sequenc

Title: Perfect score:

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OM nucleic

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Database

ALIGNMENTS

Arabidopsis thalia Arabidopsis thalia Cotton fibre-speci Cotton fibre clone Cotton H gene and

Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; ss Enriched oligonucleotides and corresp. sequences - used as markers for human genes transcribed in-vivo, facilitate tagging of most human genes Human brain Expressed Sequence Tag EST01293. (USSH) US DEPT HEALTH & HUMAN SERVICE. Venter CJ; 93WO-US01294 92US-0837195 (first entry) Q61275 standard; DNA; 359 Moreno RF, WPI; 1993-272882/34. 12-FEB-1993; Homo sapiens 12-FEB-1992; WO9316178-A. 19-AUG-1993. Adams MD, Gene RESULT Q61275/

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Example 4; Page 465; 500pp; English.

Anti-sense strand Vector pShuttle DN Vector plasmid pCM Nucleotide Sequenc Plasmid pCisEBON f

Human secreted exp Nucleotide sequenc Epstein Barr virus Nucleotide sequenc

Q61275 A43416 A42628 V55831 A50254 A75454 X90923 V213778 V21683 V21683 V21683

352.8 245.2 206 110.6 110.6 110.6 110.6 110.6 110.6 110.6

799 1926 2580 2580 5452 8705 9600 10380

Human brain Expres Rat secreted expre

Description

DB

Length

Query

Score

Ş. Result

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The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTS which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisenes sequences, probes and constructs. EST01293 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also 059041-061440.
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Sequence 359 BP; 137 A; 57 C; 55 G; 110 T; 0 other;

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                                                       2436 tttatatacttgccttatttgaatgtttagcagtatccccttcccacttatattgtgt 2495
                                                                                                                                                                                                                                                                                       2316 atgttttaaaaagaagaagaacactgccttgattatacgaatacactcagaaagtacatttag 2375
                                                                                                                                                                          2376 cttgtagtgttgaattctcttaaaggaatgcttgaattttttcattattgttttattgtt 2435
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                  aacatacatgtaacttacataactgttaagaataacagtctgatttaataaatggt 2611
                                                                                                                                                                                                                                                            176 TTTATATACTTGCCTTATTTGAATGTTTAGCAGTATCCCCCTTCCCACTTATATTGTGT
                                                                                                                                                                                                                                                                                                                                                                            56 AACATACATGTAACTTACATAACTGTTAAGAATAACAGTCTGATTTAATAAATGGT 1
                              ö
 DB 14; Length 359;
Query Match 13.4%; Score 352.8; DB 14; Length Best Local Similarity 99.4%; Pred. No. 6.8e-74; Matches 354; Conservative 0; Mismatches 2; Indels
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A43416 standard; cDNA; 359 BP 7 RESULT A43416

A43416;

(first entry) 21-AUG-2000

Rat secreted expressed sequence tag SEQ ID NO:2156.

Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgasic; haemostatic; thrombolytic; antidialmatory; cytostatic; antibacterial; antifungal; antidialmatic; untidiatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; antidiabetic; neuroprotective; notropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; parkinson's disease; disease; duntington's disease; coagulation disorder; thrombosis; inflammatory disorder; Crohn's disease, tumour; infection; depression; psoriasis; ss. haemophilia;

WO200021990-A1

20-APR-2000

99WO-US24205. 15-0CT-1999;

(GEMY) GENETICS INST

ပ Collins-Racie LA, LaVallie ER, McCoy JM, Treacy M; Ď, Jacobs K, Merberg

Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders expressed

Claim 1; Page 612-613; 618pp; English.

Aut 261 to A43419 represent specifically claimed secreted expressed sequence tags (SESTS), isolated from human, mouse, xenopus and rat clasue sources. The SESTS can have a range of activities depending on the tissues they were isolated from The activities include: chemotactic; the tissues they were isolated from The activities include: chemotactic; antibacterial; antidiabetic; antiasthmatic; vulnerary; antidiabetic; antibacterial; antidiabetic; antiparkinsonian; antibacterial; catepopathic; neuroprotective; nootropic; antiparkinsonian; antibaciatic; osteopathic; neuroprotective; notropic; antidathmatic; vulnerary; antidicer; cerebroprotective; notropic; antidathmatic; vulnerary; antidicer; cerebroprotective; notropic antidaptics and antidabetic; antibactics; care useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (arthubodies: They may be useful for treatment of autoimmune disorders (asthma), mysolod or lymphold cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (castma), mysolod or lymphold cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (clond mopholis), inflammatory disorders (clond mopholis), inflammatory disorders (clond coll deficiencies) and psoriasis. A43420 to A43425 represent linker variants which are central cycles of the present invention.

Sequence 359 BP; 75 A; 131 C; 83 G; 70 T; 0 other;

; --Gaps ö 9.3%; Score 245.2; DB 21; Length 359; 86.3%; Pred. No. 1.7e-48; Indels 43; 0; Mismatches Best Local Similarity 86.3 Matches 271; Conservative Query Match

1516 cacceceaccaccaccyctctctgcctccacctggcattcgaccatcatcacctgtcacag 1575 41 ctctcacgccgccgccgcctctgcctcctaggcattcggccatcatcacctgtcacgg 100 g

1576 ttacagetettgeteatectecettgggetacatecaaetecatetaetgeeecaggte 1635 ŏ g

cccatgttccattaatgcctccatctcctccatcacaagttatacctgcttctgagccaa 1636 ò g

agogocatccatcaaccctacctgtaatcagtgatgccaggagtgtgctactggaagcaa agegecatecttecaecetaecegtgateagtgaegegaggagtgtgetgetggaggeea 221 1696 Q ò

1756 281 q

δ

aacgcattgaaaac 1829 1816 ò

341 agcggatcgaaaac 354

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expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifundatic; antioarhmatic; vulnerary; antiparkinsonian; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; cerebroprotective; neuroprotective; noctropic; antiparkinsonian; vaccine; autoimmune disorder; antidapressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; antema; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke;
                                                                                                                      Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                          Parkinson's disease, Huntington's disease, coagulation disorder;
                                                                                                                                                                                                                                                                   haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
tumour; infection; depression; psoriasis; ss.
                                                                                              Human secreted expressed sequence tag SEQ ID NO:1368
                       A42628 standard; cDNA; 242 BP.
                                                                                                                                                                                                                                                                                                                                                                                 99WO-US24205.
                                                                                                                                                                                                                                                                                                                                                                                                        98US-0104435
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                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                15-0CT-1999;
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                                                                      21-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacobs K,
                                               A42628;
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RESULT
            A42628
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Evans C; LaVallie ER, Collins-Racie LA, Treacy M; Merberg D,

WPI; 2000-317937/27

Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders

Claim 1; Page 450; 618pp; English.

rissue sources. The sESTs can have a range of activities depending on the tissues cheek solated from human, mouse, xenopus and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; heamatopoietic; chemokinetic; analgesic; heamostatic; thrombolytic; antinflammatory; cytostatic; antibacterial; antidiabetic; antibathactic; undinerary; antibucer; osteopathic; neuroprotective; noctropic; antiparkinsonian; antipactatic; carebopathic; neuroprotective; noctropic; antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules, which correspond to the SESTs. Proteins encoded by the SESTs of the identification and isolatical activity and raising antibodies. They may be useful for treatment of autoimmune disorders care useful an assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimmune disorders (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (cathma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. A43120 to A4312 rotay invention. A41261 to A43419 represent specifically claimed secreted expressed

Sequence 242 BP; 83 A; 52 C; 65 G; 42 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is a nucleotide sequence of the stabilising sequence-encoding insert. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula [(Glya)X(Glyb)Y(Glyc)Z]n where Glya, Glyb, Glyc are 1-6 sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr and n can be anything between 1-66 X, Y and Z need not be identical from n repeat to n repeat. Alternatively a nucleic acid encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein. The products can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; stabilising polypeptide; proteolytic degradation; resistence; half-life; autoimmune disease; inflammation; nitro drug: IkappaB regulator protein; inflammatory bowel disease; in vivo imaging: nitroreductase protein; enzyme therapy; prodrug therapy; protease;
                                                                                                                                                                                                                                                   78 gtcctcatgaaccagaaaaagtgccaagagcacctcatgacaggcggcgagaatggcaga 137
                                       Gaps
                                                                                                             21 tgcaagatacagaggataagaggaaggaaagaggaagcaga---agaaaaatctagatc 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion proteins resistant to proteolytic degradation -
comprising a core protein with a stabilising polypeptide comprising
a peptide sequence containing glycine repeats
                                                                           739 tgcaagatacagaggataagaggaaggaaagaggaagcagaagcagaaaaatctagatc
                                                                                                                                                       agetggcccaaggtccagagctggctgaagatgatgctaatctcttacataagcatattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of the stabilising sequence-encoding insert.
                                     3;
Length 242;
                                       Indels
                                                                                                                                                                                                                                                                                                             919 aagttgctaatggcccagcctctcattttgaaacaagacctc 960
                                                                                                                                                                                                                                                                                                                            ..
Query Match 7.8%; Score 206; DB 21; Best Local Similarity 98.6%; Pred. No. 2.4e-39; Matches 219; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; pathological condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 4B; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            V55831 standard; DNA; 799 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0048945.
96US-0030986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-312463/27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epstein-barr virus.
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V55831/c
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Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy -

(PHAR-) PHARMACOPEIA INC RA, Chelsky

Horlick

P-PSDB; Y95856.

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used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in
                                                                                                                                                                                                                                                 1163 ccctcagtcaccagctacaggcagaacacctgtgtttgtgagccccactccccacctcc 1222
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                                                                                                                          Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;
                                                                                                                                                                             DB 19;
                                                                                                                                                                           Score 110.6; DB 1
Pred. No. 1.4e-16;
                                                                                     diagnostic methods such as in vivo imaging.
                                                                                                                                                                             4.2%;
                                                                                                                                                                                             Best Local Similarity 50.7
Matches 266; Conservative
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EBV, nuclear antigen 1; EBNA1; episome; transfection; selection; gene therapy; ds.
                                                        Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.
A50254 standard; DNA; 1926 BP
                                                                                                                                                               11-FEB-2000; 2000WO-US03547
                                                                                                                                                                                   99US-0249585
                                      (first entry)
                                                                                                       Epstein-barr virus
                                                                                                                          WO200047778-A1.
                                     07-NOV-2000
                                                                                                                                                                                  11-FEB-1999;
                                                                                                                                             17-AUG-2000
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The present sequence is that of DNA encoding the Epstein-Barr virus (EBV) nuclear antigen protein 1 (EBNA1, see Y95856). EBNA1 is stably unclear antigen protein 1 (EBNA1, see Y95856). EBNA1 is stably transfected with at least one episome. This method involves transfecting a eukaryotic cell with: (1) a first episome comprising a first protein whose expression results in cell death and a second expression results in cell death and a second protein where expression of the second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce expression of the encoding a second protein where expression of the second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce comprising an EBV orly and a gene encoding a second protein of the first protein to produce expression of the episomes by the cells. The doubly transfected cells which also express an antigen that promotes retention of the episomes by the marker is maintained. Cransfected cells are maintained under conditions in which the first and second proteins and the selectable marker is maintained. Under these conditions, only cells containing both episomes, and the protein of interest from the other episomes, and the epitopes may further comprise a nucleic acid sequence encoding a protein of interest from the other episome. Either or both epitopes may further comprise a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence encoding as tagged or the cells. The method is applicable to cell culture or mittand establishment of eukaryotic cells that stably and reliably expressed agence of interest, using a novel method of selection, and establishment of evaluation without the need for exogenous Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other; selection factors, such as antibiotics. Disclosure; Fig 2; 53pp; English.

toctococotocagtacotococacotocacocococgottgoaagotocago 1342 |||| ||||||| | ||||| | |||| | |||| |||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 1163 ccetcagteaceagetacaggeagaacacetgtgtttgtgageeceactececactee 1222 tecaceacetettecatetgeettgteaacttecteattaagagetteaatgaetteaac 1282 Gaps agtaccaccacctccagctcctctcagattgcccctggagttcttcacccagctcctcc tecaattgeacetectetagtacageetetecaceagtagetagagetgeeceagtatg tgagactgtaccagttcatccactcccacaaggtgaagttcagggggctgcctccacccc 1 4.2%; Score 110.6; DB 21; Length 1926; Similarity 50.7%; Pred. No. 2.2e-16; 56; Conservative 0; Mismatches 259; Indels 0; Matches 266; Query Match Best Local 930 1223 1283 810 1403 1463 1343 ò à qq ò g δ q qq ò

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RESULT A75454/c

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                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Epstein Barr Virus Nuclear Antigen 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X90923 standard; DNA; 5452 BP
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98US-0130114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-610610/52
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                                                                                                                           451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition for detecting protein-protein interactions in a mammalitwo hybrid system comprises bait and test vector which consist of selection gene, vector viral origin of replication and fusion gene
               Origin of replication; protein-protein interaction; replication; two-hybrid system; nuclear antigen; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of the Epstein Barr nuclear antigen.
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50.7%; Pred. No. 2.6e-16;
.1ve 0; Mismatches 259;
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                                                                                                                                                                                                                                                                                      A75454 standard; DNA; 2580 BP.
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Best Local Similarity
Matches 266; Conserv
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Luo Y,

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plasmid pcwvBBNA from which Epstein Barr Virus Nuclear Antigen I (EBNA I) encoding DNA is obtained. EBNA I protein is used to stably maintain episomes containing EBV origin of replication (oriP) and a gene encoding protein or RNA of interest. Bucaryotic host cells expressing EBNA I protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy,
                                                                                                                                      sequence is an anti-sense strand of commercially available
  expressing genes from recombinant eukaryotic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5452 BP; 1108 A; 1736 C; 1246 G; 1362 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              for gene amplification, cell immortalisation, etc.
                                                                              Example 1; Fig 1; 86pp; English
                            gene therapy
New method
useful for
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99WO-US06742. 98US-0079792.

28-MAR-1999; 28-MAR-1998; 06-NOV-1998

07-OCT-1999

WO9950457-A1

Synthetic.

ö coctcagicaccagetacaggcagaacaccigititigigagccccactccccacctcc 1222 tecaccacctettecatetgeettgteaactteeteattaagagetteaatgaetteaac 1282 tccaattgcacctcctctagtacagccctctccaccagtagctagactgccccagtatg 1462 1523 accaccgcctcctctgcctccacctggcattcgaccatcatcacctgtcacagttacagc 1582 tottgctcatcctccttgggctacatccaactccatctactgccccaggtccccatgt 1642 tgecectectgecectectgecectectectgetectgecectectgetectgecectee 1791 1912 tectgecetectgecetectgecetectectgetectgecetectgecetecter 1971 Gaps agtaccaccacctccagctcctcttcagattgcccctggagttcttcacccagctcctcc tgagactgtaccagttcatccactcccacaaggtgaagttcaggggctgcctccacccc ö Length 5452; 259; Indels 1643 tecattaatgeetecateteetecateacaagttataectgette 1687 DB 20; .7e-16; 0; Mismatches 4.2%; Score 110.6; 50.7%; Pred. No. 3.7 Best Local Similarity 50.7 Matches 266; Conservative Query Match 1223 1552 1612 1463 1163 1283 1343 1732 1792 1403 1583 ò g ò g à q ò q ò g ò g ò 셤 à g ò

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Vector pShuttle DNA

14-JAN-2000

XEXEX

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RESULT Z23778

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This invention describes a novel method for generating an antisense library targeted to a selected RNA transcript. The methods can be used for identifying antisense agents and for identifying target sites for antisense-mediated inhibition of a selected gene. The use of a direct library for target site selection significantly simplifies the screening process, since only very small libraries need be prepared and assayed. This sequence represents the vector pShuttle which is used in the method tocaccacctcttccatctgccttgtcaacttcctcattaagagcttcaatgacttcaac 1282 cocteagteaccagetacaggeagaacacetgtgtttgtgageeceaeteeceaetee 1222 Gaps for identifying antisense for antisense-mediated cecteetgecectectgetectgecectectgecectgetectgecectectgecec tectececetecagtacetececeaectecageceaetgetttgeaagetecage tectgecectectgecectectgecectectgecectectgetectgecectec tgoccetectgetectgecectectgetectgecectectgetectgecectectgetee tccaattgcacctcctctagtacagccctctccaccagtagctagagctgccccagtatg tycocottoctyccoctcottyccoctcottyctcottyccoctcottyccoctgo tyagactgtaccagttcatccactcccacaaggtgaagttcaggggctgcctccacccc tgecectectgecectgetectgecectectgetectgecectectgecectec Length 8705; ö Sequence 8705 BP; 1875 A; 2575 C; 2078 G; 2177 T; 0 other; Indels DB 20; Score 110.6; DB 20; Pred. No. 4.7e-16; 0; Mismatches 259; Production of antisense libraries, used agents and for identifying target sites inhibition of a selected gene -Claim 16; Page 43-50; 63pp; English 2 Chen (UTAH) UNIV UTAH RES FOUND Pierce ML, WPI; 1999-610866/52. of the invention. Ruffner DE,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This polynucleotide comprises the DNA sequence of vector plasmid pCMWKmITR-EPI, which contains an Epstein-Barr virus (EBV) origin of replication from plasmid pCEP4, a coding region for EBV nuclear antigen A from pCEP4, a pair of inverted terminal repeats from adeno-associated virus, a cytomegalovirus enhancer/promoter, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polycationic agents based on alpha-amino acids, able to complex with nucleic acid - to facilitate its entry into cell, condense it and protect it against serum degradation, particularly for use in
                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/note= "CMV immediate-early enhancer/promoter"
6818..7050
                                                                                                                                                                                                                                                                                                                                                                                                                  "bovine growth hormone polyA sequence"
                 1643 tecattaatgeetecateteetecateacaagttataeetgette 1687
                                                                                                                                                 Polynucleotide delivery; plasmid pCMVKmITR-EPI; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Innis MA;
                                                                                                                                                                                                                                                                                                              /rpt_type= INVERTED
/note= "AAV inverted terminal repeat"
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'note= "AAV inverted terminal repeat"
                                                                                                                                                                                                                                                                        /*tag- b
/note- "EBV origin of replication"
4928..5104
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/product= "EBV nuclear antigen A"
                                                                                                                                                           gene therapy; vaccine; polycationic agent; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dwarki V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 77-80; 100pp; English.
                                                                                                                                                                                                                          Location/Qualifiers
14..2594
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zukermann R;
                                                                                                                                                                            Chimeric - Epstein-Barr virus.
Chimeric - Adeno-associated virus.
Chimeric - Cytomegalovirus.
Chimeric - Bos taurus.
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                                                                       V21683, standard; DNA; 9600 BP
                                                                                                                                Vector plasmid pCMVKmITR-EPI
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                                                                                                             (first entry)
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Murphy JE,
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G_i protein coupled receptor; G_iPCR; G_i_a protein; cytoplasmic calcium; calcium mobilization; nociceptin receptor; chemokine receptor; CCR3; CCR2; interleukin 8 receptor type B; episomal expression vector; ss.
bovine growth hormone polyA sequence, and a kanamycin resistance selectable marker. Polynucleotides encoding polypeptides, such as erythropoietin or leptin, and ribozymes and antisense polynucleotides can be inserted into the vector. The vector is polynucleotides can be inserted into the vector. The vector is perferred for use in novel compositions and methods for improved polynucleotide delivery into cells. In these methods, polycationic agents are used to increase the frequency of uptake of a nucleic acid (see also V2164-86) into a cell. The polycationic agent can condense with the nucleic acid and inhibit serum and/or nuclease degradation of the nucleic acid. The nucleic acid can be vector, may express a therapeutic protein or a vaccinating viral or cancer antigen, or is itself therapeutic (antisense or ribozyme). The methods and compositions can be used in the gene transpy of many diseases.
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Pred. No. 5e-16;
0; Mismatches 259;
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ID z22248 standard; DNA; 10380
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Best Local Similarity 50.7
Matches 266; Conservative
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in vitro mutagenesis;

W09947921-A1

Synthetic.

23-SEP-1999.

09-FEB-1999; 18-MAR-1998;

Damaj BB,

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/phenotype= neomycin_resistance
/note= "Tn5 neomycin phosphotransferase gene"
7975..8112
6365 recreerecerecreerecreerecreerecreerecreerecree 6321
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proteolysis resistant; liver; malignancy; CMV-driven;
Cytomegalovirus; episomal expression plasmid; ss.
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label= HSV_TK_terminator_3'-end
                                                                                                                                                                                                                            Plasmid pCisEBON for subcloning huHGF variants.
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"CMV enhancer/promoter"
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note= "family of repeats"
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/function= cloning_linker
967..1107
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1580..4189
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note= "SP6 RNA start"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= b
label= SP6_promoter
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note= "dyad region"
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/label=_TK_promoter
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/note= "SV40 poly
1108..1531
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/label= delta_2a
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295..4887
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ID 051731 standard; DNA; 10596 BP
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label= EBNA-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                protein coupled receptor (G_IPCR) and with a gene coding for a G_i_a protein capable of coupling to the G_iPCR, to increase the cytoplasmic calcium upon binding of an agonist to the G_IPCR. The cell is used to assay a test compound for its effect on a G_IPCR. The method and cells are useful for assaying agonist and antagonist compounds, which bind to G_IPCR which, stimulate intracellular calcium mobilization, such as the nociceptin receptor, and particularly chemokine receptors such as CCR3, cCR2 and the interleukin B receptor type B. The present sequence represents the nucleotide sequence of the pCEP4 vector.
                                                                                                                                                                                                                                                                                                                          A method to enhance signal transduction responses involving cytoplasmic calcium release \phantom{a}
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larity 50.7%; Pred. No. 5.2e-16;
Conservative 0; Mismatches 259;
                                                                                                                                                                                                                                             Robbins AK;
                                                                                                                                                                                                                                                                                                                                                                                          Examples; Fig 3A-J; 64pp; English.
                                                                                                                     99WO-US02852.
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                                                                                                                                                                                                    (PHAR-) PHARMACOPEIA INC
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                                                                                                                                                                                                  Hepatocyte growth factor variants - are resistant to proteolytic cleavage into its two-chain form, used to treat malignancies associated with HGF receptor
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50.7%; Pred. No. 5.2e-16;
tive 0; Mismatches 259;
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92US-0884811.
92US-0885971.
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                                                                                                                Godowski PJ, Lokker NA,
                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                         WPI; 1993-386573/48.
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    18-MAY-1992;
18-MAY-1992;
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(first entry)

09-DEC-1996

T40348;

This sequence represents the episomal CMV driven expression plasmid CC pCisEBON which was used in the expression of variant human hepatocyte pCisEBON which was used in the expression of variant human hepatocyte ciscopath factor (HGF). HGF is isolated from human serum and is a disulphide linked heterodimer derived by proteolytic cleavage of the pro-hormone between residues 494 and 495. This generates a molecule composed of an alpha subunit of 440 amino acids (mol. wt. 69 kD) and beta subunits are encoded by a single open reading frame. The alpha and beta subunits four Kringle domains based on their homology to kringle-like contains four Kringle domains based on their homology to kringle-like domains in other proteins, e.g. prothrombin, plasminogen. The beta subunit shows high homology to the catalytic domain of serine proteases contains which retain HGF. Therefore, the precise function of the beta chain remains unknown. The invention includes HGF serine proteases are not conserved in HGF. Therefore, the precise contains which retain HGF receptor binding activity without having the biological activity of wild-type HGF. They can be used for the treatment of pathological conditions associated with the activation of a HGF receptor such as malignancies associated with chronic HGF receptor activation. The proteins and proteins confined sequence and expression may be used for manipulation of the HGF coding sequence and expression confined the proteins. ö Human; hepatocyte growth factor; HGF; huHGF; serum; proteolytic cleavage; ppco hormone; beta subunit; alpha subunit; kringle domahn; prothrombin; plasminogen; catalytic domain; serine protease; HGF variant; HGF receptor; malignancy; chronic HGF receptor activation; ss. 2774 contragical accade tacad graduate and the state of the st 1343 agtaccaccacctccagctcctcttcagattgcccctggagttcttcacccagctcctcc 1402 Gaps New hepatocyte growth factor variants - are resistant to in vivo proteolytic cleavage into a 2-chain form, useful as HGF antagonists tecaccacetettecatetgeettgteaactteeteattaagagetteaatgaetteaac tectececetecagtacetececeaectecagetecagetetetgeaagetecage Length 10596; Sequence 10596 BP; 2627 A; 2571 C; 3023 G; 2375 T; 0 other; Indels pCisEBON for expression of hepatocyte growth DB 17; 4.2%; Score 110.6; DB 17; 50.7%; Pred. No. 5.2e-16; cive 0; Mismatches 259; Example 1; Fig 6; 39pp; English. Mark 93US-0087783. 92US-0884811. 92US-0884811. Lokker NA, Conservative (GETH) GENENTECH INC WPI; 1996-392634/39 Similarity Godowski PJ, 18-MAY-1992; 18-MAY-1992; Query Match Best Local Simi Matches 266; US5547856-A 20-AUG-1996 .8-MAY-1992 Synthetic. 1283 g ŏ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the nucleotide sequence of pCIS.EBON, which is used in the course of the invention. The specification describes a hepatocyte growth factor (HGF) variant (HGFV) comprising an amino acid (aa) alteration at or adjacent to position 692 of the wild-type human HGF (huHGF) as sequence. HGFV may be used in studies to identify the structure-activity relationships of HGF in order to identify the functionally important domains in the as sequence. It may also be used to identify as residues which are responsible for the interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGF with its receptor, and those as that are responsible for the biological activity of it. Variants of HGFV which have enhanced receptor biological affinity (compared to wild-type whuGF) and are more biologically active than wild type huHGF, may be used as huHGF agonists. Conversely, variants of HGFV which have enhanced receptor binding affinity (compared
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                                                                                                                                                                                                 New hepatocyte growth factor variants - useful for studying structure-function relationships in the wild type molecule and for treating conditions associated with chronic hepatocyte growth factor receptor activation
1523 accaccgcctcctctgcctccacctggcattcgaccatcatcatcgtcacagttacagc
                                                         tgagactgtaccagttcatccactcccacaaggtgaagttcagggggctgcctccacccc
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                                                                                                                                                                                                                                             pCIS.EBON; hepatocyte growth factor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
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malignancies associated with chronic HGF receptor activation.
HGFV-immunoglobulin chimeras may be produced (by standard methods) and used in protein A purification, immunohistochemistry, and immunoprecipitation techniques (in place of anti-HGF antibodies) or in screening studies to identify inhibitors of HGF-HGF interactions.
wild-type huHGF) but which are biologically inactive may be used as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreerecreer
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Pred. No. 5.2e-16;
); Mismatches 259; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10596 BP; 2627 A; 2571 C; 3023 G; 2375 T; 0 other;
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retase; beta-amyloid precursor protein; beta-amyloid plaque component; Alzheimer's disease; amyloidogenic

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The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence encodes a human beta-secretase enzyme.
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                                                                                                                                                                                                                   to discover inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                 Purified beta-secretase protein used in assays to discover inhibit which can be used for the treatment of amyloidogenic diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 110.6; DB 21; Length 16080;
Pred. No. 6.4e-16;
0; Mismatches 259; Indels 0;
                                                                                                                                     Power M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16080 BP; 3627 A; 4556 C; 3962 G; 3913 T; 22 other;
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                                                                                                                                 John V,
nloque L;
                                                                                                                        Doane MT, Frigon W, cc...
                                                                                                                                                                                                                                                                                      Disclosure; Fig 13A-E; 121pp; English.
                                                                                                                                               Tung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.2%;
              10-FEB-2000; 2000WO-US03819.
                                              99US-0119571.
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Best Local Similarity 50.77
Matches 266; Conservative
                                                                                                 (ELAN-) ELAN PHARM INC
                                                                                                                                 fp, Basi G,
Tatsuno G,
                                                                                                                                                                                   WPI; 2000-533011/48.
                                                                                                                                                                                                                                                    Alzheimer's disease
                                               10-FEB-1999;
                                                               15-JUN-1999;
                                                                                                                                 Anderson JP,
Sinha S, Ta
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The present sequence is one of a large number of 5' ESTs derived from manas encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                            Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 165 BP; 43 A; 48 C; 25 G; 49 T; 0 other;
                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 21732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 21732; 71pp + CD-ROM; English
                                                                                                                                                                                                 gene therapy; chromosome mapping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                              21-FEB-2000; 2000EP-0200610.
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                                  C17657 standard; cDNA; 165
                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                        EP1033401-A2
                                                                                                                                                                                                                                      Homo sapiens
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                                                                      C17657;
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Gaps

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Indels

Score 110.4; DB 21; Pred. No. 7.3e-17; 0; Mismatches 1;

4.28; 99.18;

Query Match
Best Local Similarity 99.1
Matches 111; Conservative

Length 165;

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caacattcacgtcctgccctataaccgattaattaattgatccccagctaga 112

Search completed: June 20, 2001, 17:22:48 Job time: 8300 sec

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Perfect score:

Sequence:

OM nucleic

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Scoring table:

Database

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1163 ccctcagtcaccagctacaggcagaacacctgtgtttgtgagccccactccccactcc 1222
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                                                                                                                                                                                                                                                                                                             Sequence 2. Application US/09050863
; Sequence 2. Application US/09050863
; GENERAL INFORMATION:
; APPLICANT: Lao, Ying
APPLICANT: Payan, Don
; TITLE OF INVENTION: System
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSS:
; ADDRESSEE: Flahr, Hobbach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                        Mammalian Protein Interaction Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 30-MAR-1998
CLASSIFICATION:
US-08-298-829-25
US-08-217-337-3
US-08-298-687A-3
US-08-298-687A-3
US-08-298-687A-3
US-08-787-335-2
US-08-306-691B-23
US-08-306-691B-23
US-08-100-730-1
US-09-100-730-1
US-09-100-730-1
US-09-100-730-1
US-09-323-735-1
US-09-323-735-1
US-09-323-735-1
US-08-557-309B-16
US-08-933-674A-16
US-08-993-674A-16
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
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Best Local Similarity 50.77
Matches 266; Conservative
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EDNESS: unknown
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US-09-050-863-2
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   STATE:
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                                                                                 June 20, 2001, 15:04:28 ; Search time 88.99 Seconds (without alignments) 5464.753 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-728-323A-1
US-08-70-379-20
US-08-757-669A-20
US-08-010-928B-1
US-08-209-747-1
US-08-458-298-1
US-08-781-891-208
US-08-232-463-14
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US-07-885-971-15
US-08-087-783A-15
US-08-194-088B-15
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PCT-US93-04648-15
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JS-09-010-928B-3
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US-08-298-687A-25
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US-08-425-069-1
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Maximum Match 100%
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-884-811-15/c; Sequence 15, Application US/07884811 patent No. 5316921; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33,055
SER: 755.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dreger, Ginger R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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COUNTRY: USA
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Best Local Similarity
Matches 266; Conserv
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1073 rececercerecererecerecerecreerecreerecreecerecreerecree 1014
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                                                                                                                                                                                                                                                                                                                          Length 5452;
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APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 086//10903US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1643 tecattaatgeetecatectecteateaagttataeetgette 1687
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50.7%; Pred. No. 3.8e-18;
:ive 0; Mismatches 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09130114
Patent No. 5976807
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Best Local Similarity 50.7'
Matches 266; Conservative
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ORGANISM: VEBNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 5.5e-18;
0; Mismatches 259;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
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Sequence 15, Application US/07885971
Patent No. 532887
Sequence 15, Application US/07885971
Sequence 15, Application US/07885971
Sequence 15, Application US/07885971
Sequence 15, Mark, Melanie R.
TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19920518
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94080
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COMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Genentech, Inc.
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                                                                                                                                                                                    Score 110.6; DB 1
Pred. No. 5.5e-18;
0; Mismatches 259
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-Jul-1993
CLASSIFICATION: 435
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08087783A Patent No. 5547856 GENERAL INFORMATION:
                                                                                                                                                                                    Query Match 4.2%;
Best Local Similarity 50.7%;
Matches 266; Conservative
SEQUENCE CHARACTERISTICS:
                     LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                            linear
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                                                                                       ; TOPOLOGY:
US-07-885-971-15
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APPLICANT: GOGOWSK1, Paul J. Lokker, Nathalie A. Mark, Melanie R.
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   Length 10596;
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                                                                                                                                                  P0755779P1
PRIOR APPLICATION L.....
APPLICATION NUMBER: 07/884811
FILING DATE: 18 wAx-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18 wAx-92
ATTORNEY/AGENT INFORMATION:
NAME: MASSCHAME, Diene L.
REGISTRATION NUMBER: 95,600
REFERENCE/DOCKET NUMBER: 95,600
REFERENCE/DOCKET NUMBER: 907557
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: 415/952-9881
TELETAX: 415/952-9881
INFORMATION FOR SEG ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 base pairs
TYPE: NUCLEIC ACIG
STRANDEDNESS: SINGLE
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                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREMY SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURREMY APPLICATION DATA:
PILING DATE: 09-FEB-1994
CLASSIFICATION NUMBER: 05/08/194,088B
FILING DATE: 09-FEB-1994
CLASSIFICATION DATA:
PRICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
ATPORNEY/ACBNT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 755D1
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEFHONE: 415/255-2614
: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEGUENCE CHARACTERISTICS:
LENGTH: 10596 bases
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                                                                      COUNTRY:
ZIP: 9408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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PCT-US93-04648-15/c
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                                                                                                                                                                                APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS CORRESPONDENCE ADDRESS: 21
ADDRESSEE: Genentack Canner 
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   0; Mismatches 259;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,087
FILING DATE: 18-MAY-1992
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                             Sequence 15, Application US/08194087
Patent No. 5879910
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFRENCE/DOCKET NUMBER: 779
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
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INFORMATION FOR SEQ ID NO: 15:
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Matches 266; Conservative
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nucleic acid
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APPLICANT: Godows
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                                                                                                           RESULT 7
US-08-194-087-15/c
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CORRESPONDENCE ADDRESS:
ADDRESS:
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21P: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

~MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Godows)
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460 Point San Bruno Blvd
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APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA: 07/885971
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
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California
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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Matches 266; Conservative
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                                                                                2473 recreecerecreecerrecreecerecreerecreerecreeceerecreecerecreerecree 2414
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APPLICANT: Fallis, Lynne
APPLICANT: Bellmare, Guy
APPLICANT: Boivin, Rodolphe
TITLE OF INVENTION: A BRASSICA REGULATORY SEQUENCE FOR
TITLE OF INVENTION: ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
                              1463 tgagactgtaccagttcatccactcccacaaggtgaagttcagggggctgcctccacccc
                                                                                                                                                            1643 tecattaatgeetecateteetecateaeagttataeetgette 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER NEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: McAndrews, Held, and Malloy STREET: 500 W. Madlson St. 34th Floor CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/915,246
FILING DATE: 19920716
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ATTORNEY/AGENT INFORMATION:
NAME: POCHOPIGEN, DORALD J.
REGISTRATION NUMBER: 32,167
REFERENCE/DOCKET NUMBER: 91 P
TELECHONICATION INFORMATION:
TELEPHONE: 312 707-8889
TELEPHONE: 312 707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/07915246
Patent No. 5401836
GENERAL INFORMATION:
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ADDRESSEE: MCANdrews
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1073 GCCTCCATTCCACGCCTCCACCTCCATGTCCACCTGCACGCCCACCT----CCATA 1017
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                                                                                                                                                                                              Length 1505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immediate Early Protein From Kaposi's
Sarcoma-Associated Herpesvirus, DNA
Encoding Same And Uses Thereof
                                                                                                                                                                                        Score 104.6; DB 1;
Pred. No. 6e-17;
0; Mismatches 259;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08728323A
Sequence 1, Application US/08728323A
Sequence 1, Sequence 2, APPLICANT: Russo, James 2, APPLICANT: Relaman, Isidore 3, APPLICANT: Relaman, Isidore 5, APPLICANT: Relaman, Isidore 5, TITLE OF INVENTION: Sarcoma-Associal 71TLE OF INVENTION: Encoding Same A TITLE OF INVENTION: Encoding Same A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                              4.0%;
51.0%;
     Brassica napus
                                                                                                                                                                                                                        Best_Local Similarity 51.0
Matches 273; Conservative
) ORGANISM: Brassica no
STRAIN: Westar
DEVELOPMENTAL STAGE:
TISSUE TYPE: Root
US-07-915-246-1
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                                                                                                                                                                                                 Query Match
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Bohenzky, Roy A.
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                                                                                                                                                                      ADDRESSEE:
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                                                              APPLICANT:
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                                          APPLICANT
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                                                                                                                                                                                        0575/52268/JPW/MSC/SKS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.7%; Score 98.4; DB 2;
49.8%; Pred. No. 3.5e-15;
tive 0; Mismatches 251;
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John.P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2269 CCTGCTGCTCTGTTCATCC 2250
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                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                           TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 49.8
Matches 249; Conservative
                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                   linear
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; LOCATION:
US-08-728-323A-1
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Sequence 20, Application US/08770379 Patent No. 5849564 GENERAL INFORMATION: APPLICANT: Chang, Yuan

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19488 GCTCCTGCTCCTCTAACTCCTGCTGCTCCTCTAACTCCTGCTCCTGCTCCTCTAACT 19547
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                                                                                FROM KAPOSI'S SARCOMA-ASSOCIATED DNA ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cttcacccagctcctcctaattgcacctcctagtacagccctctccaccagtagct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 98.4; DB 2; 49.8%; Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                         E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIR Release #1.0, 'CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                             TITLE OF INVENTION: POLYPEPTIDES TITLE OF INVENTION: HERPESVIRUS,
Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 5.7
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INPERATION FOR SEQ ID NO: 20: 20:
SEQUENCE CHARACTERISTICS:
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US-08-770-379-20
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nucleic acid
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Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P. REGISTRATION NUMBER:
                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 STATE: New York COUNTRY: U.S.A. ZIP: 10036
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3.5%; Score 93;
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-010-928B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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19668 CTAACTCCTGCTCCTCTCTAACTCCTGCTCCTCCTCCTGCTGCTCCTTCTT 19727
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                                                                                                                                                                                                                  APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Relaman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPGALLO
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELECATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 124
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                       Sequence 20, Application US/08757669A
Patent No. 6183751
                                                                                   19728 CCTGCTGCTCTGTTCATCC 19747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                   1686 tctgagccaaagcgccatcc 1705
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.7
Best Local Similarity 49.8
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                New York
: New York
                                                                                                                                                                                                           GENERAL INFORMATION:
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ZIP: 10036
                                                                                                                                                       US-08-757-669A-20
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STATE:
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"Flagelliform DNA sequence irom the 5' region. The putative start codon is at
                                                    19488 GCTCCTGCTCCTCTAACTCCTGCTCCTGCTCTAACTCCTGCTCCTGCTCCTCTAACT 19547
                                                                                                                                              19548 CCTGCTCCTGCTCCTGCTCCTGCTCCTCTAACTCCTGCTCCTGCTCCTTA 19607
                                                                                                                                                                                                                                                       19608 ACTCCTGCTCCTGCTCCTAACTCCTGCTCCTGAACTCCTGATCCT 19667
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1446 agagetgeecceagtatgtgagaetgtaceagtteateeacteecacaaggtgaagtteag 1505.
                                                                                                                                                                                                                          1566 cctgicacagitacagetettgeteateeteeetetgggetacatecaactecatetact 1625
                                                                                                                                                                                                                                                                                                                                     1626 gececaggiceceaigticeattaatgeetecatetectecateacaagtiatacetget 1685
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GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V

APPLICANT: Hayashi, Cheryl Y

TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA

TITLE OF INVENTION: CODING THEREFOR
                                                                                                              1506 gggctgcctccacccccaccaccaccgcctcctgcctccacctggcattcgaccatcatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
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position 219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: BILD GATEHOUSE RD. SUITE 500E ·
CITY: FALLS CHURCH
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/010,928B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09010928B
Patent No. 5994099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19728 CCTGCTGCTCCTGTTCATCC 19747
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NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 14
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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DB 2; Length 2830;

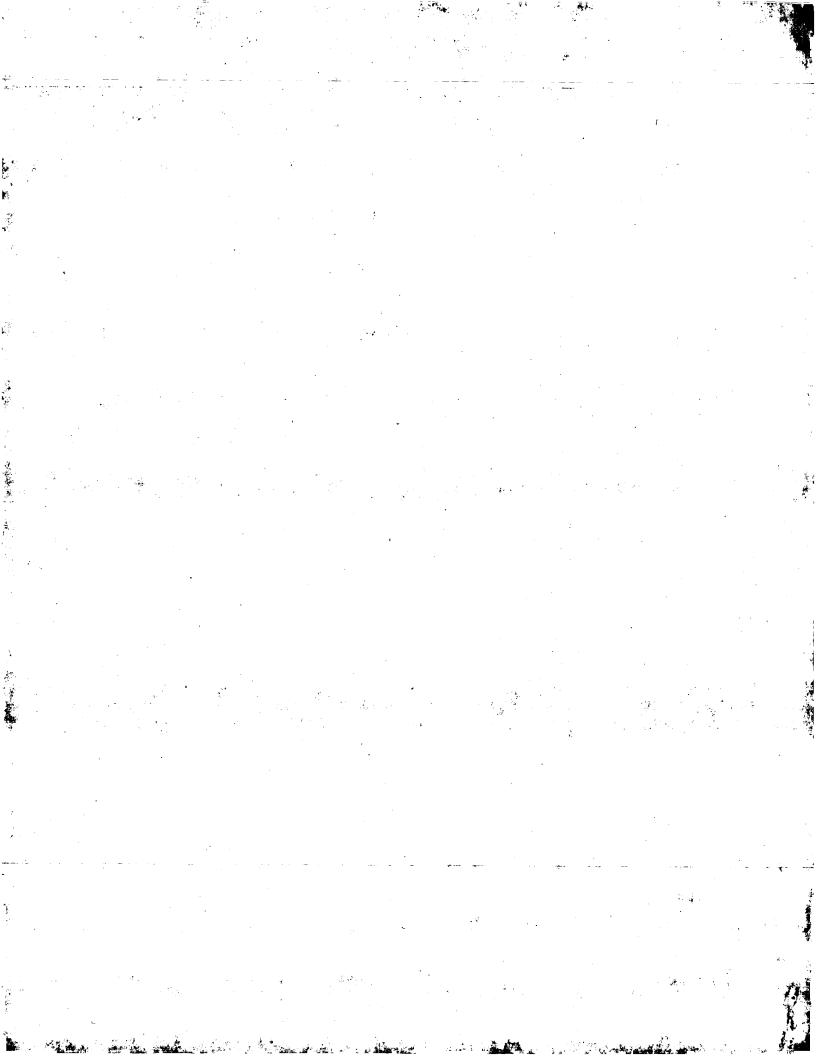
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US-08-209-747-1
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Best Local S
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                                                                                          1859 AGAGCGACCAGGTCCAACGTTTCCTGGTCCAGCACCACCGGGTCCGGAACCTCCAGCGCC 1800
                                                                                                                               1118 gatacccacctgtatcagttctgctacaggtttgatagaaaatcgccctcagtcaccagc 1177
                                                                                                                                                                  1799 TGCTCCACCGATTGTTAATTCTTCTGTATTGTTATCGGGCCATCTGCACCATCAATTGT 1740
                                                                                                                                                                                                                                         1739 AATATCCAAATCCTCTACGATGTTGTGCGCCGGGATCCTCCTGCTCCACCAGCACCTCC 1680
                                                                                                                                                                                                                                                                                1238 atctgccttgtcaacttcctcattaagagcttcaatgacttcaactcctccccctccagt 1297
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                                                                                                                                                                                                          tacaggcagaacacctgtgtttgtgagccccactcccccacctcctccaccacctcttcc
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7.2e-14;
ches 325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
CITY: Falls Church COUNTER: USA
ZIP: 22040-3487
Pred. No. 7.2e); Mismatches
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APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding
TITLE OF INVENTION: Silk Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/209,747
FILLING DATE: 14-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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Patent No. 5733771
GENERAL INFORMATION:
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47.0%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Local Similarity 47.0
hes 288; Conservative
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CORRESPONDENCE ADDRESS:
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1905 GCAGCGCCTCCAGCTCCTGCTCCAGCAGCTGCCGCAGCACCAGCTCTTGCTCCGGCAC-- 1846
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OTHER INFORMATION: /product= "N. clavipes minor OTHER INFORMATION: ampullate silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91.2; DB 1;
Pred. No. 2e-13;
0; Mismatches 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
            ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGIGSTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5%;
                                                                                                                                                                                                                                                                                    LENGTH: 2793 base pairs
TYPE: nucleic acid
                                                                                                                                                                                        TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nes 296; Conservative
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CLASSIFICATION:
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Pred. No. 2e-13;
0; Mismatches 293; Indels 9
                                       GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: 511k Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: /product- "N. clavipes minor OTHER INFORMATION: ampullate silk protein" US-08-458-298-1
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                   SEE: Birch, Stewart, Kolasch & Birch : P.O. Box 747 Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/458,298 FILING DATE: 02-JUN-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,747
ELLING DATE: 14-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 1, Application US/08458298
Patent No. 5756677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%;
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703-205-8050
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Best Local Similarity 49.5'
Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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183..2675
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STREET: P.O
CITY: Falls
STATE: Virg
COUNTRY: US
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June 20, 2001, 15:04:28; Search time 1943.75 Seconds (without alignments) 12765.911 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

2200 2260 α g ò a ò a ð 셤 1 (bases 1 to 851) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope

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ö 1899 2079 2379 1900 atgaagtagattggttggagtaagaaaatgcattgataaatattacaaaactgaatgca 1959 1720 taatcagtgatgccaggagtgtgctactggaaagcaatacgaaaaggtattcagctacgca 1779 1780 aagtagaagagcagcgtgaacaggaagctaagcatgaacgcattgaaaacgatgttgcca 1839 420 180 300 009 0; Gaps 1840 ccatcctgtctcgccgtattgctgttgaatatagtgattcggaagatgattcagaatttg 541 GAAATTGAAATCTTGAGGGCAGCTGTATCTACTAATGAGCCTTATTCCATTTCCTGATGT : www.genoscope.cns.fr 32.2%; Score 844.6; DB 105; Length 851; 99.2%; Pred. No. 9.1e-188; cive 4; Mismatches 3; Indels 0; Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www. /organism="Homo sapiens" Location/Qualifiers Matches 844; Conservative Best Local Similarity Query Match source BASE COUNT ORIGIN 2080 FEATURES ð g 음 q g Q qq ò ò

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
acttatatattgtgtgatatgatttgcttgcttgctataggagttaaaaacttttccatgtg 2540
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                         atgaagtagattggttggagtaagaaaatgcattgataaatatacaaaactgaatgca 1959
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                                                                                                                                                                                           Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                             Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Ull,W.B., Gruber,C., Jessee,J. and Mammalia;
Unpublished (2001)
Contact: Genoscope
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                              TAATCAGTGATSCCAGGAGTGTGCTACTGGAAGCAATACGAAAAGGTATTTCASYACGCA 839
                                                                                                                                                                                                                                                                                          AL526602 898 bp mRNA EST 13-FEB-2001
AL52602 LTI_NFL003_NBC3 Homo sapiens CDNA clone CS0DC020Y018
prime, mRNA sequence.
AL52602.1 GI:12790095
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Pred. No. 5.9e-155;
9; Mismatches 50; Indels 19.
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/lab_host="DH10B"
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| 158 c 135 g 276 t 10
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BP 191 91006 EVRx cedex - France
Email: segrefégenoscope.cns.fr, Web : www
Location/Qualifiers
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Best Local Similarity 91.3%;
Matches 819; Conservative
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ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix.Research Institute.
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Pred. No. 2.1e-145;
0; Mismatches 10;
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a 183 c 141 g 167 t
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/organism="Homo sapiens"
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Best Local Similarity 98.1%;
Matches 682; Conservative
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Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwing Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNN and cDNA amplification were performed under
low stringency conditions."
80 a 157 c 158 g 223 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC3&t2=RC3-HT0230-
201199-013-c11&t3=1999-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 712.

1. 718
AW379048 718 bp mRNA EST 04-FEB-2000
RC3-HT0230-201199-013-c11 HT0230 Homo sapiens cDNA, mRNA sequence.
AW379048
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 969
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Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates, Catarrhini; H
1 (bases 1 to 718)
HCGP http://www.ludwig.org.br/ORESTES.
The PAPESP/LICR Human Cancer Genome Project
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95.5%; Pred. No. 1.1e-139;
cive 0; Mismatches 25;
                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
                                                                     GI:6883707
                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung, Vector: pDNR-LIB (Clontech); Site_1:
Sfil (gyccgcctcggcc); Site_2: Sfil (gyccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor: sequence: 5'-ACAGGCCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGGGCCCATGG-GT(30)BN-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                cctcagacatacgtggatcatatggatggatcttactcactttctgccttgccatttagt 1016
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
High quality sequence stop: 726.
Liceation/Qualiflers
                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4655351"
/clone_lib="NIH_MGC_59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                   agccaaagcgccatccatcaaccctacctgtaatcagtgatgccaggagtgtgctactgg 1749
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Pred. No. 1.3e-134;
0; Mismatches 41;
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Best Local Similarity 93.1
Matches 747; Conservative
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Hegde, P., Qi,R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holi, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
          EST375443 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                       DB 122; Length 636
                                                                                                                                        a model of
                                                                                                                                  Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray Unpublished (2000)
The Institute for Genomic Research 7712 Medical Center Dr., Rockville, MD 20850, USA 7712 Medical Center Dr., Rockville, MD 18350, USA 7713: 301 838 9528
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/db.xref="taxon:9606"
/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptSKm"
125 c 140 g 164 t
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98.7%; Pred. No. 2.5e-133;
iive 0; Mismatches 7;
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                              AW963370.1 GI:8153206
                                                                                                                                                                                                                            Email: johnq@tigr.org
Plate: 187
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Matches 628; Conservative
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El (bases 1 to 98)

National Institutes of Health, Mammallan Gene Collection (MGC)

National Institutes of Health, Mammallan Gene Collection (MGC)

Ontact: Robert Strausberg, Ph.D.

Email: Gapbbs-rfmail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CLONG distribution: MGC clone distribution information can be found distribution: MGC clone distribution: MGC clone distribution with Library MGC clone distribution: MGC clone distr
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/lab_host="DH10B (phage-resistant)"
/note="Coran: bone; Vector: pcWv-SpORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for full:length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Pred. No. 2.8e-132;
0; Mismatches 34; Indels 10;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4369058"
/clone_lib="NIH_MGC_86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG111973 988 bp mRNA
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Best Local Similarity 94.1%;
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 aagcagaagcagaaaaatcta-gatcgtcctcatgaaccagaaaaagtgccaagagcacc
                                                                                                                                                                                     tgctaatctcttacataagcatattgaa---gttgctaatggcccagcctctcattttga
                                                                                                                  AAGCAGAAAAAATCTATGATCGTCCTCATGAACCAGAAAAGTGCCAAGAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 652)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10409 row: m column: 04
High quality sequence stop: 638.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/organism="Homo sapiens"
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/clone="IMAGE:457163"
/clone=lib="NHH_MGC_93"
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/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                          ctgtatcagttctgctacaggtt 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG288785
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654
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COMMENT

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
1 (bases 1 to 650)
Hedde, P., Oi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
1.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
   pCMV-SPORT6; Site_1: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW956469 650 bp mRNA EST 01-JUN-2000
EST368539 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
AW956469 GI:8146152
                                                Technologies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: bladder; Vector: pCMV-SPORT6; Site_Site_2: Sall; Cloned unidirectionally; oligo-dT Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Techn Note: this is a NIH_MGC_Library."
                                                                                                                                                                             5;
                                                                                                                                            Score 605.2; DB 175; Length Pred. No. 1.5e-131; Mismatches 13; Indels
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al Similarity 97.3%;
638; Conservative
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MO 63108

BASE COUNT

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FEATURES

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size-selected for >0.5 kb inserts and has an average insert size estimated at 1.2 kb. This library was constructed using the CAP-trapper method for full-length enrichment and has not undergone amplification. Library was constructed by Dr. Claudio Schneider (LNCIB-Area
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi:

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 540)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,

J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White Y., Wylie,T., Waterston,R. and Wilson,R.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: brain; Vector: pBluescript SK (Stratagene); vsite_1: SstI; Site_2: Xnoi; Double-stranded cDNA was prepared from human fetal brain tissue. 5' and 3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
au65f06.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone
IMAGE:2519651 3', mRNA sequence.
A1928895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 TCTTAATTGTGTACTTTGTGAATTTTAATTTAAAGAAAGCAACTGAAATTGAAATCTTGA 361
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5'-GAGAGAGACTCGAGTTTTTTTTTTTTTT-3'.
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/organism="Homo sapiens"
/organism="taxon:9606"
/clone="IMAGE:2519651"
/clone_lib="Schneider fetal brain 00004"
/sex="male"
                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
444 Forest Parkway, Box 8501, St. Louis,
11: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="frontal lobe"
/dev_stage="5 months post-conception"
/lab_host="DH10B"
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Pred. No. 1.6e-113;
0; Mismatches 1;
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Best Local Similarity 99.8
Matches 529; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                            Assessment of gene expression patterns in a model of metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tal: 301 838 3528
Fax: 301 838 0208
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1. .650
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAG/none_lib="MAGE resequences, MAG/none_lib="Vector: plluescriptsKm"
a 120 c 124 g 207
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Pred. No. 2.8e-122;
0; Mismatches 32;
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ilarity 94.6%;
Conservative (
                                                                                                                                                                            Email: johnq@tigr.org
Plate: 92
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG176906 835 bp mRNA EST 06-FEB-2001
602313474F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4419042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nh.gov

Insue Procurement: Louis Staudt, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can liquid through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM10154 row: d column: 19
                                                                                                                                                                                                                                                                                      tcattgcaagaacgtgtggaccgtttatctgttagtgttacacagcttgatccaaaggaa
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 835)
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/db_xref="taxon:9606"
/clone="IMAGE:4419042"
/clone_lib="NIH_MGC_85"
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:3841135"
/clone=lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="blu108 (phage-resistant)"
/note="Organ: placenta; Vector: POTB7; Site_1: XhOI;
/note="Organ: placenta; Vector: POTB7; Site_1: XhOI;
/note="Organ: placenta; Vector: POTB7; Site_1: XhOI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGACGGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 727)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM532 row: e column: 08
High quality sequence stop: 669.

1. 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A EST 15-SEP-2000 sapiens cDNA clone IMAGE:3841135
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Pred. No. 2e-109;
0; Mismatches 28; Indels 3;
                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE731111 727 bp mRNA 601566327F1 NIH_MGC_21 Homo
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94.7%;
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Best Local Similarity 94.7
Matches 551; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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human.

SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

ACCESSION VERSION KEYWORDS

DEFINITION

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FEATURES

BASE COUNT ORIGIN

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/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                         615 tacgatgttt-gtgaacagcctccacctctcaatatactcactccttatagagatgatgg
                                                                                                                                  25;
                                                                                                               Length 835
                                                                                                                                  Indels
                                                                                                             Score 510.6; DB 174;
Pred. No. 2.8e-109;
0; Mismatches 49; In
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91.0%;
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Best Local Similarity 91.0
Matches 745; Conservative
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RESULT

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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library Noricash_GG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 147592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 746 Std Error: 0.00
Seq primer: -400P from Gibco.
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Tissue Producmement: Christopher A. Moskaluk, M.D., Ph.D., Mi
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrat;
Mammalia; Eutheria; Primates; Catarrhini; Hominid;
1 (bases 1 to 497)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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100.0%; Pred. No. 6.6e-106;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
          mRNA
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          AW071606 497 bp
wt94a11.x1 NCI_CGAP_GC6
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Similarity 98.3 32; Conservative
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0230-040
500-ll10-f02xt13-2000-05-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under lus stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                              l (bases I to 55).
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Sllva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., W.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                               HT0230 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                         257 ATTTAGCTTGTAGTGTTGAATTCTCTTAAAGGAATGCTTGAATTTTTTTATTGTTTT 198
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AUTHORS
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DB 164; Length 555;

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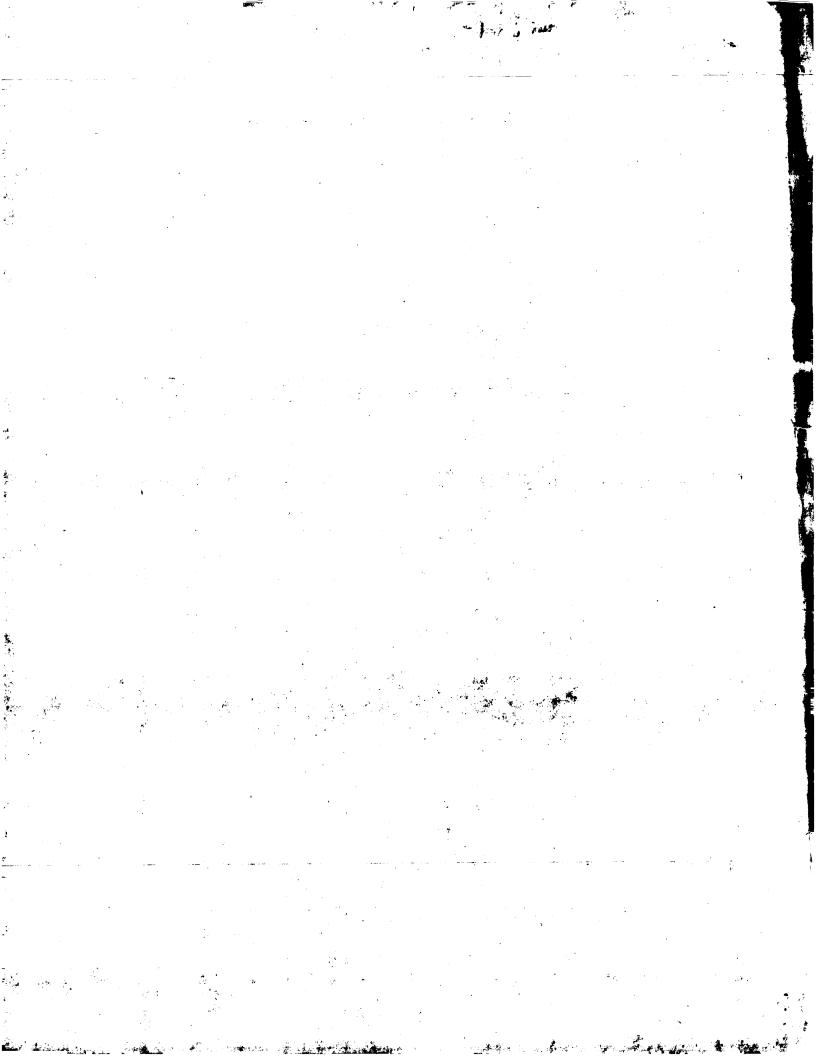
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Query Match

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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                 Gaps
                                                                                 5 ACGGTGTTCTGGCACAAGGTT-ATCTCAAGA-GCCGCTAGTGAAAAGAAACATCGATCC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                        Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                 3,
                 Indels
Pred. No. 9.4e-106;
0; Mismatches 6;
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Animal Genetics Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV664100 547 bp
AV664100 Bos taurus brais
5', mRNA sequence.
AV664100 (GI:9923130
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a 95 c 198 g 134 t 2 others
                                                                                                                                                                                                                                                                                                              atccactcccacaaggtgaagttcaggggctgcctccaccccaccaccgcctcctctgc 1539
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Pred. No. 2.5e-105;
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rattus norv rattus norv

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095763 homo sapien Q9z0g8 rattus norv

mus musculu

Q9vkm2 drosophila

rattus norv

homo sapien

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Q9h0a2 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20428428; PubMed-10970852; Westphal R.S., Soderling S.H., Alto N.M., Langeberg L.K., Scott J.D.; Scottyhal R.S., soderling S.H., Alto N.M., Langeberg L.K., Scott J.D.; ScottyAvRell, a wishott-aldrich syndrome protein, assembles an actin-associated multi-tinase scaffold."; EMBO J. 19:4589-4600(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANIIRQLSSLSKYAEDIFGELFNEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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SEQUENCE 559 AA; 61508 MW; 8746910987D80D16 CRC64;
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Best Local Similarity 100.
Matches 218; Conservative
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                 Mus musculus (Mouse)
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09wze9 homo sapien
09w2r5 drosophila
09myl6 macaca neme
09prd5 gallus gall
09nuz7 homo sapien
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                                                                                                                                                                     425026 seqs, 132305027 residues
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        GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                             protein search, using sw model
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09UPY6
09UDY7
060794
09WXE9
09WZR5
09WZR5
09WZR5
09WZR5
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Gapop 60.0 , Gapext 60.0
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Q9YMX1
Q9Q5L3
P70433
Q9XUV2
Q9ES67
Q9ES67
                                                                                                                                                                                                                                                                                                                                                             sp_phage:*
sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
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.: sp_archea:*
:: sp_bacteria:*
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Maximum DB seq length: 200000000
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559
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InterPro; IPR002965;
InterPro; IPR003124;
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Matches 22; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                       MEDLINE-98402540; PubMed-9732292;
Bear J.E., Rawls J.F., Saxe C.L. III.;
"SCAR, a WASP-related protein, isolated as a suppressor of receptor defects in late Dictyostellum development.";
J. Cell Biol. 142:1325-1335(1998).
                                                                                                                Homo sapiens (Human).
Usukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.4e-16;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Machesky L.M., Insall R.H.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO20707; BAA4923.1: -.
EMBL; AF134305; AAD33054.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6135C2160991E8BB CRC64;
                                                                        (TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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                                                              Created)
                                         PRT;
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MEDLINE-99310608; Pubmed-10381382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 PSYFFDLWKEKMLQDTEDKRKEKR 177
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02205; WH2; 1.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00246; WH2; 1.
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01-MAY-2000 (TrEMBLrel. 13, Cr
01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2001 (TrEMBLrel. 16, La
WASP-FAMILY PROTEIN.
                                                                                            KIAA0900 PROTEIN (FRAGMENT).
KIAA0900.
                                         PRELIMINARY;
                                                             (TrEMBLrel. 10,
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                                                             01-MAY-1999
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01-MAR-2001
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SEQUENCE
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Bear J.E., Rawls J.F., Saxe C.L. III.;
"SCAR, a WASS-related protein, isolated as a suppressor of receptor defects in late Dictyostellum development.";
J. Cell Biol. 142:1325-1335(1998).
Suetsugu S., Miki H., Takenawa T.; "Identification of two human WAVE/SCAR homologues as general actin regulatory molecules which associate with the Arp2/3 complex."; Biochem. Blophys. Res. Commun. 260:296-302(1999).
EMBL, AB026543; BAA81796.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ393P12.2 (HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 LIKE)
                                                                                                                                                                                                                                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Machesky L.M., Insall R.H.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR134304; ARD33053.2; -.
InterPro; IPR002965; -.
                                                                                                                                                                         PERMIT PF02205; WH2; 1.
PRINTS; PR01217; PRICHEXTENSN.
SWART; SM00246; WH2; 1.
SEQUENCE 502 AA; 55411 MW; 140DD58309345F35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 AA; 53963 MW; 8A9D97D0D964734F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        Score 24; DB 4; L
Pred, No. 4.8e-16;
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100.0%; Pred. No. 5.7e-14;
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0; Mismatches
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PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00246; WH2; 1.
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Best Local Similarity 100.0
Matches 24; Conservative
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NON_TER SEQUENCE

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Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO002965; BAA91064.1; InterPro: JERRO29655; -.
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                       22657 MW; FC1E09F8AE83C082 CRC64;
                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ20289 FIS, CLONE HEP04492.
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Pred. No. 0.00068;
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100.0%; Pred. No. v.
0; Mismatches
210 AA
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SEQUENCE FROM N.A.
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01-OCT-2000
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                 09NXE9;
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Suetsugu S., Miki H., Takenawa T.;
Identification of two human WAVE/CAR homologues as general actin
regulatory molecules which associate with the Arp2/3 complex.";
Biochem. Biophys. Res. Commun. 260:296-302(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 5.7e-14;
ive 0; Mismatches 0; Indels
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                                                                                                                     Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AA022578; CAA18609.1; -. InterPro; IRR003124; -. Pfam; PF02205; WH2; 1.
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SMART; SM00246; WH2; 1.
SMART; SM00246; WH2; 1.
                                                                                                                                                                                                             497 AA; 54062 MW; 58872599FDF63A6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
WASP-FAMILY PROTEIN (DJ144C9.2).
                                                                                                                                                                                                                                                                                                                                                                                                                               498 AA
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100.0%; Pred. No. 5.7
ive 0; Mismatches
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PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
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Submitted (FEB-2000) to the EM
EMBL; AB026542; BAA81795.1; -.
EMBL; AL096774; CAC18518.1; -.
InterPro; IPR002965; -.
InterPro; IPR002066; -.
InterPro; IPR003124; -.
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Best Local Similarity 100.0
Matches 22; Conservative
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Length 210; 0; Indels

A MEDLINE—20196006; PubMed=10731132;

A Mamarides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,

A Mamarides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,

A Mamarides P.G., Scherer S.E., Holf R.A., Evans C.A., Galle R.F.,

A Mamarides P.G., Scherer S.E., Holf R.A., Evans C.A., Chen L.X.,

A Maria G., Worturan J.R., Yandell M.D., Zhang O., Chen L.X.,

B Erandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

A Marii J.F., Agbagani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

B Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

B Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

A Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

A Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

A Berkova D., Botcher A., Deng Z., Mays A.D., Daw I., Ditex S.M.,

A Ghodson K., Doup L.E., Downes M. Dugan-Rocha S., Dunkov B.C., Dunkov B.,

Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Alalali M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A.,

KRA Kimmel B.E., Kodira C.D., Kraft C., Kranitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Drosophila melanogaster (Fruit fly). Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Last sequence update)
Last annotation update)

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Query Match

Best Loc Matches

us-09-425-501-2.oli.rspt

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09PTD5
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Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Nelson D.R., Siden-Kiamos I., Sandard J., Puri V., Reese M.G.,
Relnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Snith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Snith T.,
Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.-Y., Wassarman D.A., Welnstock G.M., Weissenbach J.,
Millams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu C., Zheng L.,
The genome sequence of Drosophila melanogaster.";
Glibs R.A., Myers E.W., Rubin G.M., Venter J.C.;
R. Enbl., Re03452, Zab-255521.
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Macaca nemestrina (Pig-tailed macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca mulatta (Rhesus macaque).
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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2.1%; Score 12; DB 5; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 12; Conservative 0; Mismatches 0; Indels
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Kiril Y., Inoue T., Yoshino K.;
"Pig-tailed monkey Eas ligand mRNA, complete cds.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-M.fascicularis; STRAIN-CYNOMOLGUS MONKEY; K1111 Y., Inoue T., Yoshino K.; "Cynomolgus monkey Pas ligand mRNA, complete cds "; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                         239 AA; 26175 MW; 81EEE85DD2FC5FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
FAS LIGAND.
                                                                                                                                                                                                                                                PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                     FlyBase; FBgn0034551; CG15225.
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NCBI_TaxID=9545, 9541, 9544;
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202 PPPPPPPLPPP 213
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TISOBE-PLACENTA;

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TISOBE-PLACENTA;

TISOBE T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugiyamo S., Yoshikawa Y.,

Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,

Matsantar Y., Nagahari K., Masuho Y., Sasaki N.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO01891; BAA91564.1;

TIRTEPPC; IPR002965;

TIRTEPPC; IPR002965;

PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KIAA0009 PROTEIN.
Gallus gallus (Chicken).
Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                   Length 280;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                        Indels
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Castagnola P., Tonachini L., Monticone M.;

"CDNA cloning of chick KIAA0009.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF208489; AAF2114.1;

InterPro; IPR001799;
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                              2.1%; Score 12; DB 6; Lk
100.0%; Pred. No. 0.00088;
ative 0; Mismatches 0;
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                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                  PD002533;
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NCBI_TaxID=9031;
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InterPro; IPR003124; -.
Pfam; PF02205; WH2; 3.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
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        DNA Res. 7:273-281(2000).
EMBL; AB046818; BAB13424.1;
NON_TER 1 1
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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268 PPPPPPLPPPG 279
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344 PPPPPPPLPPP 355
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                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10449;
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Q9YMX1
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Q9Q5L3
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Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;
Prediction of the coding sequences of unidentified human genes.
XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP 41547 MW; CD0749C6AF02BD74 CRC64;
                                                                                                                                                                                                                                                                                                                                Ender F., Hallmann A., Amon P., Sumper M.; "Response to the sexual pheromone and wounding in the green alga Volvox: induction of an extracellular glycoprotein consisting almost
                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                Volvox carteri f. nagariensis.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
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           2.1%; Score 12; DB 4; Length 360; llarity 100.0%; Pred. No. 0.0011; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TEMBLrel. 16, Last annotation update)
KIAA1598 PROTEIN (FRAGMENT).
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J. Biol. Chem. 274:35023-35028(1999).
EMBL; AJ242540; CAB62280.1; -.
InterPro; IPR000216; -.
InterPro; IPR002966; -.
                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                           STRAIN=HK10;
MEDLINE-20044763; PubMed=10574980;
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PRINTS; PRO1218; PSTLEXTENSIN.
PRINTS; PRO0239; RHODOPSNTAIL.
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                                                                        424 PPPPPPPPLPPP 435
Query Match
Best Local Similarity
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01-MAR-2001
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SEQUENCE FROM N.A.
MEDLINE-99124785; PubMed=9887315;
Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
Slavicek J.M., Rohrmann G.F.;
Slavicek J.M., Rohrmann G.F.;
Slavicek J.M., Rohrmann G.F.;
Vannicia dispar.,
Virology 253:17-34(1999).
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01-MAY-2099 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ESSENITAL STRUCTURAL FOOTEIN PP78-81
Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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                                                                          Length 446;
                                                                                                                            Indels
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF081810; AAC70187.1; -.
InterPro; IPR001005; -.
InterPro; IPR002965; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00246; WH2; 1.
SEQUENCE 555 AA; 61055 MW; 6B638D6E02279887 CRC64;
SEQUENCE 446 AA; 51473 MW; 5C82402E11E75570 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
EBNAZ-LIKE PROTEIN.
                                                     Score 12; DB 4; Ler
Pred. No. 0.0013;
                                                          2.1%; Scor.
100.0%; Pred. No. c.
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MEDLINE-20057932; PubMed-10590127;
MA MEDLINE-20057932; PubMed-10590127;
MA HAYWARD G. S., Tan J., Ling P.D.;
That Hayward G.S., Tan J., Ling P.D.;
The Sequence and functional analysis of EBNA-LP and EBNA2 proteins from the nohuman primate lymphocryptoviruses.";
J. Virol. 74:379-389(2000).
MR EMBL; AR200187; AAF22206.1; -.
MR EMBL; AR200187; AAF22206.1; -.
MR InterPro; IPR0005955; -.
MR InterPro; IPR0005955; -.
MR INTES; PR01217; PRICHEXTENSN.
MR PRINTS; PR001217; PRICHEXTENSN.
MR PRINTS; PR00806; VINCULIN.
MR PRINTS; PR00806; VINCULIN.
MR SEQUENCE 605 AA; 64712 MW; AD0F77111208AA4E CRC64;
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirine; Lymphocryptovirus.
NCBI_TaxID=104228;
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Search completed: June 20, 2001, 12:14:38 Job time: 197 sec

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Query Match 2.1%; Score 12; DB 14; Length 605; Best Local Similarity 100.0%; Pred. No. 0.0017; Matches 12; Conservative 0; Mismatches 0; Indels

4.5 Compugen Ltd.	
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	
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protein search, using sw model OM protein June 20, 2001, 12:10:01; Search time 22.54 Seconds Run on:

(without alignments) 1889.156 Million cell updates/sec

1 MPLVKRNIDPRHLCHTALPR.....AVEYSDSEDDSEFDEVDWLE 559 US-09-425-501-2 559 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Word size :

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOMERNIES	
Result No.	Score	Query	Query Match Length	DB	ID	crip
н	12		281	7	I38707	Fas ligand - human
7	12	2.1	389	7	S27200	proline-rich prote
e	12	2.1		7	T30349	structural protein
7	12	2.1	-	7	T23252	hypothetical prote
5	11	2.0	433	N	T07910	rolin
9	11	2.0	477	7	I38409	adenylyl cyclase-a
7	11	2.0	662	7	D40228	
80	11	2.0	798	~	D96563	
6	11	5.0		~	S19595	
10	11	5.0	٦.	~	T09073	splicing factor Si
11	11	2.0	1	~	T00063	hypothetical prote
12	10	1.8		N	T46186	hypothetical prote
13	10	1.8	145	~	T48552	glutaredoxin-like
14	10	1.8		7	D41132	collagen-related p
15	10	1.8		7	T30760	hypothetical prote
16	10	1.8	185	7	B26669	nodulin-20 precurs
17	10	1.8	207	7	I53154	scleraxis - mouse
18	10	1.8	211	7	S28304	
19	10	1.8	275	7	T02559	probable spliceoso
20	10	1.8	367	7	S02193	
21	10	1.8		7	T34018	hypothetical prote
22	10	1.8		7	S41318	 hypothetical prote
23	10	1.8		7	B85187	+
24	10	1.8		7	JC4386	
25	10	1.8	551	7	A60047	
26	10	1.8	681	N	JC5929	serine/arginine-ri
27	10	1.8	691	~	T46476	
28	10	1.8	907	N	663	hypothetical prote
53	10	1.8	1058	N	T13286	cappuccino gene pr

formin related pro- cyclic-nucleotide diaphanous-related unknown protein [i formin isoform IV diaphanous protein hypothetical prote formin mouse hypothetical prote alpha-fetoprotein hypothetical prote AcMNPV orf91 - Bom probable proline-r probable proline-r probable proline-r probable proline-r probable proline-r produlin-20a - soyb	
713963 A48508 C86441 C86441 C324607 T31065 S48375 S48375 A41948 T77126 E96750 T41831 H83120 T07735	
1064 1108 1120 1200 1255 1255 1255 1268 12783 1300 1300 1310 1310 1310	
000000000000000000000000000000000000000	

ALIGNMENTS

RESULT

			C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-20		s.		A; Title: Human Fas ligand: gene structure, chromosomal location and spec	
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			ange		; Nac		tion	
			t ch		Ē,		loca	
			#tex		Suda		mal	
			8661		E+		DSOMO	
			May-]	4	Abe,		chr	
			-67	C; Accession: I38707; JC2340; S57565; I38554	R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.		ure,	260
			isior	55; 1	awa,		truct	A; Reference number: I38707; MUID:95127560
			rev	S575	Inaz	994	ne s	UID:
		C; Species: Homo sapiens (man)	ence	140;	Σ.	Int. Immunol. 6, 1567-1574, 1994	l: ge	7; M
) sua	#sedn	JC23	aka,	7-157	igand	13870
	an	sapie	866	707;	Tan	156	as l	er:
	Fas ligand - human	Omo	lay-1	138	Ē	9	an F	qunu
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138707	Fas	C;S	C;D	C; A	R, T	Int	A; T	A; R

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on and species specifici

A; Status: preliminary; translated from GB/EMBL/DDBJ

A.Cross-references: EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431
R;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Blocham. Bloch A; Molecule type: mRNA A; Residues: 1-281 <RES>

A. Accession: JC2340
A. Molecule type: DNA
A. Molecule type: DNB38122; DDB3:D29820; NID:g601892; PIDN:BAA07320.1; PID:g136990
R. Schatzlein, C.E.
R. Schatzlein, C.E.
A. Molecule type: MNA
A. Residues: 1-281 < CCH>
A. Cross-references: EMBL:X89102; NID:g887455; PID:g887456
A. Cross-references: EMBL:X89102; NID:g887455; PID:g887456
A. Thile: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A. Reference number: I38554; MUID:95105731

A; Accession: I38554

A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: manA A,Residues: 1-281 <RE2> A,Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628

A;Introns: 151/1; 116/3 C;Keywords: glycoprotein; transmembrane protein F:80-102/Domain: transmembrane #status predicted <TMM> F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

ö Gaps ö Query Match 2.1%; Score 12; DB 2; Length 281; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 12; Conservative 0; Mismatches 0; Indels

Thu Jun 21 10:57:42

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R;Yu, G.; Swiston, J.; Young, D. J. Cell Sci. 107, 1671-1678, 1994
A;Title: Comparison of human CAP and CAP2, homologs of the yeast adenylyl cyclase- as A;Reference number: I38409; MUID:95051124
A;Accession: I38409
A;Gene: CESP:KO2E2.2
A;Map position: 5
A;Introns: 41/1; 79/3; 131/3; 197/1; 262/1; 297/3; 566/3; 610/3; 735/3; 775/3; 834/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1-31/Domain: signal sequence #status predicted <SIG>F;32-433/Product: hydroxyproline-rich glycoprotein GAS29 #status predicted <MAT>
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A;Molecule type: mRNA
A;Residues: 1-433 <ROD
A;Cross-references: EMBL:AF015884; NID:g2384729; PIDN:AAB69863.1; PID:g2384730
A;Experimental source: gametes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydroxyproline-rich glycoprotein GAS29 precursor - Chlamydomonas reinhardtii C;Species: Chlamydomonas reinhardtii C;Species: Chlamydomonas reinhardtii C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1995 C;Accession: T07910 R;Rodriguez-Martinez, H.; Haring, M.A.; Von Gromof, E.; Beck, C.F. submitted to the EMBL Data Library, July 1997 A;Reference number: 216207 A;Reference number: 216207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Spēcies: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C;Accession: 138409
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A;Molecule type: mRNA
A;Residues: 1-477 <RES>
A;Cross-references: EMBL:U02390; NID:9409928; PIDN:AAA20587.1; PID:9409929
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                                                                                                                                                     Length 1021
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A;Cross-references: GDB:9957118
C;Superfamily: adenylyl cyclase-associated protein MCH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%; Score 11; DB 2; Le Local Similarity 100.0%; Pred. No. 0.022; Les 11; Conservative 0; Mismatches 0;
                                                                                                                                                        DB 2; I
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Pred. No. 0.02;
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0; Mismatches
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                    348 PPPPVPPPPPP 359
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                                                                                                                                                                                                                                                                     R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria of
A;Reference number: 220836; MUID:99124785
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C;Species: Genochabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T2325
R;Lloyd, C.
R;Lloyd, C.
R;Eference number: 219716
A;Reference number: 219716
A;Ref
                                                                                                                                                                                                                                                        structural protein pp78-81 - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMMEV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T30349
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: EMBL:AF081810; PIDN:AAC70187.1
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Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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      424 PPPPPPPPPPP 435
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268 PPPPPLPPPG 279
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                                      A; Molecule type: DNA
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R;Steinmeyer, K.; Ortland, C.; Jentsch, T.J.
Nature 354, 301.304, 1991
A;Title: Primary structure and functional expression of a developmentally regulated s A;Reference number: 519595; MUID:920665954
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DNA Res, 4, 307-313, 1997
A;Title: Prediction of the coding sequences of unidentified human genes. VIII.
A;Reference number: 214084; MUID:98116655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF030234; NID:g2822459; PIDN:AAC39565.1; PID:g2822460
A;Experimental source: HeLa cells
C;Keywords: pre-mRNA splicing
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T09073
splicing factor Sipl - human
splicing factor Sipl - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T09073
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00063
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Mohl. Cell. Biol. 18, 676-684, 1998
A.Title: Sipl, a novel RS domain-containing protein essential for
A.Reference number: 216554; MUID:98107652
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Pred. No. 0.043;
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100.0%; Pred. No. 0.059;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 0.05;
iive 0; Mismatches
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                 C; Superfamily: CBS homology
C; Keywords: transmembrane protein
F; 830-877/Domain: CBS homology <CBS>
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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Matches 11; Conservative
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                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-994 <STE>
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                                                                                                           C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: D4028; S77888
R:Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
Science 257, 50-56, 1992
A:Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recept A:Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recept A:Accession: D40228
A:Acteus: preliminary; nucleic acid sequence not shown A:Accession: D4028
A:Accession: D40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Reference plant Arabidopsis.
A;Reference type: DNA
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S19595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable bZIP protein, 48652-45869 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96563
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100.0%; Pred. No. 0.035;
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0.03;
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Best Local Similarity 100.
Matches 11; Conservative
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les 11; Conservative
                                                                                           neurexin II-beta precursor
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22 LPPPPPPPLP 32
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Search completed: June 20, 2001, 12:12:03
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100.0%; Fire
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Best Local Similarity 100.
Matches 10; Conservative
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A;Note: MC158R
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M.Alternate names: protein F14F18.100
M.Alternate names: protein F14F18.100
M.Alternate names: protein F14F18.100
M.Alternate names: protein F14F18.100
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: 20-Apr-2000 #sequence_revision 20-Apr-2000
C.Accession: T48552
M.Accession: T48552
M.Reference number: 224490
M.Reference number: 224490
M.Reference number: 224490
M.Reference protein Sequence Database, April 2000
M.Residus: preliminary
M.Molecule type: DNA
M.Residus: 1-145 < CREV>
M.Residus: 1-145 < CREV
M.Residus: 1
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D41132
colladgen-related protein 4 - Hydra magnipapillata (fragment)
colladgen-related protein 4 - Hydra magnipapillata
c)Species: Hydra magnipapillata
C;Species: Hydra magnipapillata
C;Date: 05-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 01-Dec-2000
C;Accession: D41113; S21932
R;Kurz, E.M.; Holstein, T.W.; Petri, B.M.; Engel, J.; David, C.N.
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thes 0; Indels
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100.0%; Pred. No. 0.0
iive 0; Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                   1315 PPPPPPLPPP 1325
425 PPPPPPPPPP 435
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Length 182;

1.8%; Score 10; DB 2; Length 182 100.0%; Pred. No. 0.086; tve 0; Mismatches 0; Indels

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J. Cell Biol. 115, 1159-1169, 1991
A; Title: Mini-collagens in hydra nematocytes.
A; Reference number: A41132; MUID:92064646
A; Accession: D41132
A; Status: preliminary
A; Molecule type: mg/MA
A; Molecule type: mg/MA
A; Residues: 1-72 < KUR>
A; Cross-references: EMBL: X61048; NID:99452; PIDN:CAA43382.1; PID:99453
A; Note: the authors translated the codon GGT for residue 142 as Pro, and TTA for residue; submitted to the EMBL Data Library, July 1991
C; Superfamily: unassigned collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: T30760
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host A; Accession: T30760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 158R - Molluscum contagiosum virus 1
N;Allernate names: MOL58R
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: U60315; PIDN: AAC55286.1
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424 PPPPPPPPLPPP 435
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Best Local Similarity
Matches 12; Conserv
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US-08-810-453-2
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COUNTRY:
                                                                                                                                                                                                                                                                                                                    US-08-810-453-2
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                                                                         June 20, 2001, 12:09:11 ; Search time 13.93 Seconds (without alignments) 808.388 Million cell updates/sec
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                                                                                                                                                             1 MPLVKRNIDPRHLCHTALPR.......AVEYSDSEDDSEFDEVDWLE 559
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Sequence 35
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Sequence 39
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                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
            Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-179-558-66
US-08-602-999A-320
US-08-762-753-39
US-08-602-999A-358
US-08-602-999A-358
US-08-545-196B-21
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                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-028-327-3
US-09-189-035-5
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                 193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                        Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                           Scoring table:
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ence 3, Appli	ence 3, Appli	ence 68, Appl	ence 68, Appl	ence 7, Appli	ence 7, Appli	7,	7, 1	ence 7, Appli	ence 9, Appli	ence 7, Appli		ence 48, Appl	ence 1, Appli	ence 2, Appli	ence 2, Appli	ence 2, Appli	ence 8, Appli	
Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	
US-09-026-587-3	US-09-227-420-3	US-09-120-365-68	US-09-515-039-68	US-08-452-722-7	US-08-404-731A-7	US-08-344-227-7	US-08-503-226B-7	US-08-721-458B-7	US-08-574-959A-9	US-08-574-959A-7	US-08-545-860D-48	PCT-US94-04496-48	US-09-157-420-1	US-08-588-985-2	. US-08-971-988-2	US-07-945-283-2	US-08-457-273B-8	
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88 9	6 62				33 9		35 9	36 9	37 9	38 9	39 9	40 9	41 9	42 9	43 9	44 9	45 9	
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ALIGNMENTS

RESULT

19.40-810-43-2

| Sequence 2, Application US/08810453
| Sequence 10. S5858990
| GENERAL INFORMATION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF TITLE OF INVENTION: FROLIFERATIVE DISORDERS
| VINNERS OF SEQUENCES. 2
| CORRESPONDENCE ADDRESS: ADDRESSE: Wolf Greenfield 6 Sacks, P.C. STREET: Federal Reserve Plaza, 600 Atlantic Avenue COUNTRY: 10 Socton 1 Reserve Plaza, 600 Atlantic Avenue COUNTRY: 10 SOCTON PROPERTY OF COMPATION AND STREET: MACOUNTRY PREADABLE FORM: COMPATION NO SATEM: PCOSY/MS-DOS SOCTON PREED TO COMPATION NO SATEM: PCOSY/MS-DOS SOCTON PREED TO COMPATION NO MARE: DATEMENT NO MARIE: BATCATION NUMBER: US/08/810,453
| CLASSIFICATION NUMBER: 36,637 |
| REGISTRATION NUMBER: 36,637 |
| RECENTING DATE: RELIZABETH R. RECISTRATION NUMBER: 3500 |
| TELECOMMUNICATION INFORMATION: NO SATEMENT OF SA

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Gaps

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TARGETING DNA METABOLIC PROCESSES USING
                                                               Length 281;
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                                                                                                                                                                                                                                                                                                   ; Sequence 2. Application PC/TUS9500362
; GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVAVION: Ligand That Binds Fas Antigen
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hockensmith, Joel W.
APPLICANT: Muthuswami, Rohini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TARGETING DNA METABOLIC PROCI
                                                               Score 12; DB 4; LA
Pred. No. 0.00091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; L
                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/00362
FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,138
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,559
FILING DATE: 01-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66, Application US/09179558; Patent No. 6180612; GENERAL INFORMATION:
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                                                             Query Match 2.1%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1
Best Local Similarity 100.
Matches 12; Conservative
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US-09-179-558-66
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PCT-US95-00362-2
US-09-290-640-25
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APPLICANT: Dean, Micholas M.
APPLICANT: Marcusson, Elic G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0351
CURRENT PAPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                           APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
TITLE OF INVENTION: Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Enbarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 12; DB 3; L
100.0%; Pred. No. 0.00091;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTORNEY APENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REFENCE/DOCKET NUMBER: 011823-006710US
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/815,190A FILLING DATE: 11-MAR-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09290640 Patent No. 6204055 GENERAL INFORMATION:
                                                             Sequence 2, Application US/08815190A Patent No. 6046310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 281 amino acids
amino acid
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Best Local Similarity 100.
Matches 12; Conservative
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-815-190A-2
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ORGANISM: Homo sapiens
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                                         US-08-815-190A-2
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APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Levitan, Irwin B.
TITLE OF INVENTION: Mechanism for the Regulation of Ion
TITLE OF INVENTION: Channel Activity
FILE REFERENCE: BRU96-02
CURRENT APPLICATION NUMBER: US/08/769,745
CURRENT APPLICATION NUMBER: 1996-12-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Score 11; DB 2; L
100.0%; Pred. No. 0.00089;
ive 0; Mismatches 0;
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100.0%; Pred. No. 0.0
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Patent No. 6184205

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.

APPLICANT: THORN, Judith M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/08769745
Patent No. 5955259
                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.0
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-602-999A-320
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 PPPPPPPPLPP 434
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-08-602-999A-409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-769-745-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 39
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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100.0%; Pred. No. 0.001;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FOWIKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: COCUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCYDOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (122)760900
TELEFER: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 09/060,470
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                              ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1155 Avenue of the Americas
                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,558
FILING DATE: 27-0CT-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 320, Application US/08602999A Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPARKS, Andrew B.
KAY, Brian K.
THORN, Judith M.
QUILLIAM, Lawrence A.
DER, Channing J.
FOWLKES, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-179-558-66
        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 PPPPPPPPPPP 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: New York
FRY: U.S.A.
10036-2711
                                                                                      New York
NY
                                                                                                                                 usa
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                                                                                                       STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
CORRESPONDENCE: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAID.

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBAM PC compatible

COMPUTER: IBAM PC compatible

COMPATIC SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNDER: US/08/545,196B

FILING DATE: 19-OCT-1995

FILING DATE: 19-OCT-1995

--AATION: --AATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP STREET: PO BOX 747 CITY: FALLS CHURCH
                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10; DB 4; Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.8%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 0.C Matches 10; Conservative 0; Mismatches
                                                                      NUMBER: US/08/602,999A
16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 22,350
REFERENCE/DOCKET NUMBER: 2121-110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 21, Application US/08545196B; Patent No. 6080577
                                                                                                                                  CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELEPANONE: (212) 790-9090
TELEPAN: (212) 869-9141/8864
TELEFX: 66141 PENNIE
TINFORMATION FOR SEQ ID NO: 358:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-602-999A-358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-545-196B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 PPPPPPPLP 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-545-196B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: POWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME.
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 10; DB 4; Length 18; 100.0%; Pred. No. 0.0055; ...
                   APPLICANT: DER, Channing J.
APPLICANT: FOWIKES, Dama M.
APPLICANT: FOWIKES, Dama M.
APPLICANT: FOREX, Dames E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FBE-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misorck, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U. SA..
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 358, Application US/08602999A Patent No. 6184205
QUILLIAM, Lawrence A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 409:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide US-08-602-999A-409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-602-999A-358
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                                                                                                                                                                                                                                                                                                                                                Length 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09382086
Fatent No. 6201106
GENERAL INFORMATION:
APPLICANT: Vue, Henry
APPLICANT: COTIEY, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFRENCE: PF-0638 US/09/382,086
CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT FILING DATE: 1999-08-24
EARLIER PAPLICATION NUMBER: 09/189,035
SARLIER FILING DATE: 1998-11-10
NUMBER OF SEQ. ID NOS: 6
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                            Score 10; DB 3;
Pred. No. 0.14;
                      APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REPERENCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/189,035
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prea. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08906360
Sequence 1, Application US/08906360
Sequence 1, Application US/08906360
GENERAL INFORMATION:
APPLICANT: Meruelo, Daniel
APPLICANT: Pampeno, Christine
TITLE OF INVENTION: MAMMALIAN HUMAN FXI-T1
                                                                                                                                                                                                                                                                                                                                 1.8%; Scu.
100.0%; Prr
0;
                                                                                                                                                                                                                                                       ; FEATURE: -
; OTHER INFORMATION: 92245671
US-09-189-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: 92245671
US-09-382-086-5
                                                                                                                                                                                                                                                                                                                                            Ouery Match 1.8
Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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364 SPTPPPPPP 373
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                                                                                                                                                                               SEQ ID NO 5
LENGTH: 480
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LENGTH: 480
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US-09-382-086-5
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                                                                                                                                                                                                                 TYPE: PRT
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             Length 288;
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DB 3; Le.,,
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0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,327
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Noil C.
APPLICANT: Guegler, Nail J.
TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 10; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
             1.8%; Score 10; DB 100.0%; Pred. No. 0.0 Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                E: Incyte Pharmaceuticals, Inc 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0482 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09189035 Patent No. 6020165
                                                                                                                                                                                                               Sequence 3, Application US/09028327
Patent No. 6130064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 96,749
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
STRANDEDNESS: single
           Query Match 1.8°
Best Local Similarity 100°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: - PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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CLONE: 1857114
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US-09-189-035-5
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CURRENT APPLICATION NUMBER: US/08/906,360
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0465 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFRAX: 650-845-4166
                  CURRENT FILING DATE: 1997-08-05
EARLIER APPLICATION NUMBER: 60/023,173
EARLIER FILING DATE: 1996-08-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 539
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US-09-016-000-2
; Sequence 2, Application US/09016000
; Patent No. 5962232
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CLONE: 307624
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Search completed: June 20, 2001, 12:11:35 Job time: 144 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Human mRNA

AF134303 D87459

JOURNAL DNA Res. 3 (5), 321-329 (1996) FEATURES Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Clone="Haf051" Clone="Haf051" Clone="Haf051" Clone="Haf051" Clone="KiAA0269" CDS 243. 1922 Gene="KiAA0269" Ado_xref="KiAA0269" Ado_xref="Gi:1665805" Ado_xref="Gi:1665805" At ranslation-"MPLKRNIDPRHICHTALPRGIKNELECVTNISLANITRQLSSL SKTARDIFFEERPAHGSFENDELSEYDONESPPELLFRANGERFYTARPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORELFRANGERFYTARPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORELFRANGERFYTARPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORELFRANGERFYTARPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYVDHAGSYRORENFERPPPERF SKTARDIFFEERPHESPSTANGLERPOTYSPARPPPPERF SKTARDIFFEERPHESPSTANGLERPOTYSPARPPPPPERF SKTARDIFFEERPHESPSTANGLERPOTYSPARPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP	Ouery Match 100.0%; Score 2625; DB 91; Length 2625; Best Local Similarity 100.0%; Pred. No. 0; Matches 2625; Conservative 0; Mismatches 0; Indels 0; Ga 1 cttctcttgcacttgcggatgatgaactggaataacgatgaaagaaa	61 121 121 181 181 241	301 301 361 361 421 421	
G19661 human STS A AF290877 Mus muscu AC019100 Homo sapi AB010070 Arabidops COntinuation (2 of AC073822 Mus muscu AL07382 Mus muscu AL07382 Mus muscu AL073823 Mis et ung AF094570 Rice tung AF094570 Rice tung AF094570 Rice tung AF094571 Rice tung AF094571 Rice tung AF094573 Rice tung AF094573 Rice tung AF094570 Rice tung AF094571 Rice tung AF06784 Homo sapi	0.8 15080 80 AL358856 AL358856 HOMO 0.8 157080 80 AL358856 HOMO 0.8 158581 80 AL359384 AC007050 HOMO 0.8 163998 86 AC007050 AC07050 AC007050 HOMO 0.8 163954 69 AC025990 AC025990 HOMO 0.8 166549 69 AC025990 AC025990 HOMO AC025990 HOMO AC025990 HOMO AC025990 HOMO 0.8 166549 69 AC025990 AC025990 HOMO AC025990 HO	DB D87459 2625 bp mRNA PRI 10-JUL-1997 QY Human mRNA for KIAA0269 gene, complete cds. D87459.1 GI:1665804 KIAA0269.1 GI:1665804 Homo sapiens male brain cDNA to mRNA, clone_lib:pSPORT 1 Clone:HA6751. Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Db Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Nomitary Direct Submission Submitted (27-AUG-1996) to the DDBJ/EMBL/GenBank databases. Nobuo Nomitary. Kazusa DNA Research Institute, Gene Structure 1: 1532-3 Nomitary. Kazusa DNA Research Institute, Gene Structure 1: 1532-3 Nama, Kisarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:0438-52-3930, Fax:0438-52-3931) Nagase,T., Seki,N., Ishikawa,K. and Nomura,N. Prediction of the coding sequences of unidentified human genes.VI. The coding sequences of 80 new genes (KIAAA0200) deduced by analysis of CDNA clones from human cell line KG-1 and brain Unpublished (1996) 3 (sites) Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,	enes. VI.

RESULT 1 D87459 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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TITLE

541	CTTCCGAAGTICTACAATTCAAGACCAGCAGTTTTCGATCGCAAGACTTTGCCTATTC 600 CATTACAGAGGACGAACTTTTCGATCGAAGACTTTGCCTATTC 600 CATTACAGAGGAGACGAACTTTTCGATCAAACTTTGCCTATTC 600	QY Ob	1621 CTACTGCCCCAGGTCCCCATGTTCCATTAATGCCTCCATCTCCTCCATCACAAGTTATA 1681 ctgcttctgagccaaagggccatccatcaaccctacctgtaatcagtgatgccaggagt	GTTATAC 1680 aggagtg 1740 AGGAGTG 1740
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	gcaga 78 GCAGA 78	Qy	1801 aggaagctaagcatgaacgcattgaaaacgatgttgccaccatcctgtctcgccgtatt. 	B-0
	tgaca 84 GACA 84	Qy		
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1561 catcacc 1561 CATCACC	catcactgtcacagttacagctcttgctcatcctcctgggctacatccactccat 1620 	RESUL AF134 LOCUS		4-JUN-1999
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LVQPSPPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPPLPPGIRPSSPVTVTALAH
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                                                                                                                                                                                  WASP,
                                                                                                                                                                                                                                                                                                                                                                                                                    /function-"activates dendritic nucleation of actin
flaments by the Arb2/3 complex.
/note-"MASP-family protein; WAVE; similar to Dictyc
suppressor of cyclic-AMP receptor"
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C (Dassa 1 to 1758)
Machesky, L. M. and Insall, R. H.
Scarl and the related Wiskott-Aldrich syndrome protein, Wak
regulate the actin cytoskeleton through the Arp2/3 complex
Curr. Biol. 8 (25), 1347-1356 (1998)
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                                                   Hominidae;
                                        Vertebrata;
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                                   Eukaryota, Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Primates; Catarrhini; L (bases 1 to 1758)

Bear, J.E., Rawls, J.F. and Saxe, C.L. III.

SCAR, a WASP-related protein, isolated as defects in late Dictyostelium development J. Cell Biol. 142 (5), 1325-1335 (1998)
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100.0%; Pred. No. 0;
ive 0; Mismatches 0;
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Machesky, L.M. and Insall, R.H.
Direct Submission
Submitted (12-MAR-1999) Blochemistry,
                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1758
                                                                                                                                                                                                                                                                                                 Birmingham B15 2TT, England
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               /gene="KIAA0269"
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Best Local Similarity 100.
Matches 1758; Conservative
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                                                                      Corby, N.
Direct Submission
Submitted (10-ARR-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (10-ARR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 9, 2001 this sequence version replaced gi:13446548.
                                                                                                                                                                                                                                     1621 GTTGAATATAGTGATTCGGAAGATGATTCAGAATTTGATGAAGTAGATTGGTGGTGGAGTAA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1681 GAAAAATGCATTGATAAATATTACAAAACTGAATGCAAATGTCCTTTGTGGTGCTTGTTC 1740
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 toacctgtcacagttacagctcttgctcatcctcccttgggctacatccaactccatct
                                                                                                                                                gettetgagecaaagegecatecateaacectaectgtaateagtgatgeeggagtgtg
                                                                                                                                                                                                                  1743 ctactggaagcaatacgaaaaggtattcagctacgcaaagtagaagagcagcgtgaacag
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                    1321 TCACCTGTCACAGTTACAGCTCTTGCTCCTCCTCCTCTGGGCTACATCCAACTCCATCT
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Catarrhini; Hominidae;
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 149944 bases at least Q40
Consensus quality: 150676 bases at least Q30
Consensus quality: 150962 bases at least Q20
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pieces.
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Insert size: 148237; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site: http://www.sanger.ac.uk
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Mammalia; Eutheria; Primates;
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Homo sapiens chromosome 6
PROGRESS ***, 6 unordered
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a 'working draft' sequence. It currently contigs. The true order of the pieces

NOTE: This is consists of 6

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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1823 tgaaaacgatgttgccaccatcctgtctcgccgtattgctgttgaatatagtgattcgga
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92318: contig of 31053 bp in length
92418: gap of 100 bp
102427: contig of 10009 bp in length
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116713. 133242
/note="assembly_fragment:01038
fragment_chain:1"
133343. 151580
/note="assembly_fragment:00639
fragment_chain:1
clone_end:17
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fragment_chain:1"
92419. .102427
/notes"assembly_fragment:01149
fragment_chain:1"
102528. .116612
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fragment_chain:1"
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/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-181P4"
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/note="assembly_fragment:01866
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                                                                                           DD 100719 TTCCCCCTGAAAAGACTAATTTGGTCAAATAAACCACTAAGTATTAAGCATGGACAGCTG 100660
                                                                                                                                                                                    DD 100659 TTGTTAGAGTAGCAGATTCAGTTTTTGATATGTTAATTGTGTACTTTGTGGATTTTT 100600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 100419 TTGTTTTATTGTTTTTATATACTTGCCTTATTTGAATGTTTAGCAGTATCCCTTCCCAC 100360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 100299 ATACTCTGACTTAAACATACATGTAACTTACATAACTGTTAAGAATAACAGTCTGATTTA 100240
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 192017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttgttttattgtttttatatacttgccttatttgaatgtttagcagtatccccttcccac 2482
                                                                                                                                                            2183 ttgttagagtagcagattcagttttttgatatatcttaattgtgtactttgtgaatttta 2242
                                                                                                                                                                                                                                                                                                                                                                                                                                            aaagtacatttagcttgtagtgttgaattctcttaaaggaatgcttgaattttttcatta 2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttatatattgtgtgatatgattttgcttgcctataggagttaaaaacttttccatgtgaa 2542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NA HTG 14-APR-2001
clone RP11-403119, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 187117 bases at least Q40 Consensus quality: 188982 bases at least Q30 Consensus quality: 190116 bases at least Q20

    Project Information

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PROGRESS ***, 11 unordered pieces.
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Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summary Statistics
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KEYWORDS
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sum-of-contigs Quality
                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* This contignous contignous properties of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* A 712 4811 contignous properties of 100 bp. A 712 4812 gap of 100 bp. A 712 4812 gap of 100 bp.
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100 bp
19575 bp in length
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80484 126461: contig of 45978 bp in length
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14085 bp in length
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/note="assembly_fragment:02427
fragment_chain:2"
.163068...10242
/note="assembly_fragment:01301
fragment_chain:2"
                       coverage: 4.74x in 020 bases; agarose-fp
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/note="sssembly_fragment:01747
fragment_chain:1"
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/note="assembly_fragment:00630
fragment_chain:1"
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'ragment_chain:1"
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//note="assembly_fragment:00226
fragment_chain:3"
177921. .184396
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/note="assembly_fragment:01664
fragment_chain:1"
126562 . 129107
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'ragment_chain:2"
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ragment_chain:2"
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fragment_chain:3"
Quality coverage: 4.85x in Q20 bases;
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/db_xref="taxon:9606"
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148782: contig of
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162967: contig of
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15691 80383: cont
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BASE COUNT ORIGIN

1823

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Homo sapiens chromosome 6 clone RP11-181P4, WORKING DRAFT SEGUENCE, 32 unordered pieces.
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143812)
                                                                                                                                                                                                                                       Center, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                       Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway,
MO 63108, USA
On Jul 7, 2000 this sequence version replaced gi:8567974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 125690 bases at least Q40
Consensus quality: 130641 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 140712; sum-of-contigs
Quality coverage: 2.84 in Q20 bases; sum-of-contigs
Quality coverage: 3.15 in Q20 bases; sum-of-contigs
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Sequencing vector: plasmid; 0%
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AUTHORS
TITLE
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note="assembly_name:Contig14"
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8668. 10333
/note="assembly_name:Contigl8"
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/note="assembly_name:Contig21"
17955. 20526
/note="assembly_name:Contig22"
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446. .2816
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note="assembly_name:Contig15"
613. .8567
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28307. .32673
/note="assembly_name:Contig25"
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note="assembly_name:Contig19"
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note="assembly_name:Contig20"
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/note≕"assembly_name:Contig23"
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/note≕"assembly_name:Contig24
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/db_xref="taxon:9606"
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/note="assembly_name:Contig43"
130373. :143812
/note="assembly_name:Contig44"
27942 c 28670 g 42684 t :
                                                  'note="assembly_name:Contig27"
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/note="assembly_name:Contig30"
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/note="assembly_name:Contig31"
55257. .60671
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/note="assembly_name:Contig32"
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/note="assembly_name:Contig33"
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/note="assembly_name:Contig34"
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/note="assembly_name:Contig35"
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86936. .91556
/note="assembly_name:Contig38"
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/note="assembly_name:Contig39"
97040. .103443
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109774. 118660
/note="assembly_name:Contig42"
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/note-"assembly_name:Contig12"
2917. 4030
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/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                          DNA HTG 07-JUL-2000
6 clone RP11-181P4, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 143812)
           141587 TTCGACCATCATCACCACATTACAGCTCTTGCTCATCCTCTCTGGGCTACATC 141646
                                                                  141647 CAACTCCATCTACTGCCCCCAGGTCCCCTTTAATGCCTCCATCTCCATCAT 141706
                                                                                                                      ttegaccateateacetgteacagttacagetettgeteatecteectetgggetacate
                                                    caactccatctactgccccaggtccccatgttccattaatgcctccatctccatcac
                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO 63108, USA
On Jul 7, 2000 this sequence version replaced g1:8567974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer ET: 100% of reads
Chemistry: Dye-primer ET: 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 125690 bases at least 0.40
Consensus quality: 130641 bases at least 0.20
Consensus quality: 133684 bases at least 0.20
Insert size: 151000; agarose-fp
Insert size: 140712; sum-of-contigs
Quality coverage: 2.84 in 0.20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0181P04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1345: contig of 1345 bp in length
1445: gap of unknown length
2816: contig of 1371 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                        ----- Genome Center ----
                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                           AC021847.6 GI:8954243
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector: plasmid;
                                                                                                                                                                                                                                                      AC021847 143812 bp
Homo sapiens chromosome
32 unordered pieces.
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JOURNAL
                                                  1612
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KEYWORDS
SOURCE
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COMMENT

14-APR-2001: *** SEQUENCING IN

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50670 AGGCACTTGTGCCACACACACTGCCTAGAGGCATTAAGAATGAACTGGAATGTAACC 50511
                                               333 aatatttccttggcaaatataattagacaactaagtagcctaagtaa 379
                                                                                                                                            ALS90549 192017 bp DNA HTG
Homo sapiens chromosome 6 clone RP11-403119,
PROGRESS ***, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Summary Statistics
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 192017)
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HTG; HTGS_PHASE1.
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AUTHORS
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5257. 60671
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                 Sims,S.
Direct Submission
Direct Submission
Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 17, 2001 this sequence version replaced gi:13625115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye: 100% of reads Consensus quality: 187117 bases at least Q40 consensus quality: 188982 bases at least Q30 consensus quality: 190116 bases at least Q20 Insert size: 191017; sum-of-contigs Insert size: 195674; agarose-fp quality coverage: 4.85x in Q20 bases; sum-of-contigs Quality coverage: 4.74x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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4812 15590: contig of 10779 bp in length
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15691 80388: contig of 64693 bp in length
80384 80483: gap of 100 bp
80484 126461: contig of 45978 bp in length
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148782: contig of 19575 bp in length
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26562 129107: contig of 2546
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177921 184396: contig of
184397 184496: gap of
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Gaps

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Indels

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0; Mismatches

Matches 167; Conservative Similarity

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Query Match Best Local

6.4%; Score 167; DB 66; Length 143812; 100.0%; Pred. No. 1e-80;

213 aggtgaactggcacaaaggttaatctcaagatgccgctagtgaaaagaaacatcgatcct 272

273 aggcacttgtgccacacagcactgcctagaggcattaagaatgaactggaatgtgtaacc 332

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Dipublished

Signary

Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,

Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S.,

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Collymore, A., Gooke, P., Dererlano, E., Garad-Diez, Galagan, J.,

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R.,

Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,

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O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,

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Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,

Schupback, R., Santos, R., Schupers, S., Schupback, R., Seaman, S., Severy, P.,

Scugnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A.,

Wilson, B., Wu, X., Waman, D., Ye, W. J., Young, G., Zainoun, J.,

Sembek, L., Zimmer, A. and Zody, M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 25, 2001 this sequence version replaced gi:13194331.

All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                       Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This record contains 75 individual

* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p of 100 bp contig of 711 bp in length p of 100 bp contig of 731 bp in length p of 100 bp contig of 714 bp in length
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contig of 710 bp in length
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8146: contig of 756 bp in length
Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 62537)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo Sapiens chromosome 11, clone RP11-55506
Unpublished
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2423 3132; cont
3133 3222; gap of
3233 3943; cont
3944 4043; gap of
4044 4774; cont
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5588: co
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7290: co
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 aggcacttgtgccacacagcactgcctagaggcattaagaatgaactggaatgtgtaacc 332
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HOMO Sapiens Chromosome 11 clone RP11-55506 map 11, LOW-PASS
SEQUENCE SAMPLING.
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100.0%; Pred. No. 1e-80;
tive 0; Mismatches 0; Indels 0;
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                    7 192017: contig of 7521 bp in length. Location/Qualifiers
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a 37927 c 37166 g 58039 t
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                                                                                                                                                                       /clone="RP11-403I19"
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HTG; HTGS_PHASE0.
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Best Local Similarity 100.0
Matches 167; Conservative
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                       184497
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ORIGIN
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KEYWORDS
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47 8246: gap of 100 bp
8962: contig of 716 bp in length
63 9062: gap of 100 bp
63 9904: contig of 742 bp in length
98 904: gap of 100 bp
1046: contig of 742 bp in length
47 10746: gap of 100 bp
17 11616: gap of 100 bp
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5: contig of 773 bp ...
100 bp ...
698 bp in length
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1726 bp in length
100 bp
of 714 bp in length
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rf 719 bp in length
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if 738 bp in length
100 bp
if 747 bp in length
100 bp
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if 745 bp in length
100 bp
if 737 bp in length
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f 783 bp in length
100 bp
f 785 bp in length
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714 bp in length
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100 bp
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706 bp in length
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19834: contig of 779 bp in length
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729 bp in length
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716 bp in length
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770 bp in length
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763 bp in length
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808 bp in length
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f 686 bp i
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32364: contig of 719 bp
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1 17298: contig of 7
9 17398: gap of 10
9 18145: contig of 7
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4 23129: contig of 7
0 23229: gap of 10
0 23974: contig of 7
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28950: contig of
29050: gap of 1
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16460: contig of
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18955: contig of
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24811: contig of
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25705: contig of
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26531: contig of
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18294 38393: gap of 1
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; gap of
31545:
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34132: cont
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22313: cont
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33247: cont
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35002: cont
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Homo sapiens sap
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55852: contig of 734 bp in length
55952: gap of 100 bp
56712: contig of 760 bp in length
56812: gap of 100 bp
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STS; STS sequence; primer; sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         713 bp in length
100 bp
745 bp in length
in length
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human STS A001U21, sequence tagged site.
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100 bp
'3 bp j
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716 bp i
100 bp
698 bp i
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707 bp 1
100 bp
769 bp 1
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717 bp 1
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730 bp 1
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771 bp 1
100 bp
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714 bp
100 bp
738 bp
                    63: gap of 100 bp
39983: contig of 720 bp
83: gap of 100 bp
40804: contig of 721 bp
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801 bp
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739 bp
                                                                                                      p of 100 bp
contig of 785 bp
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42519: contig of 730.bp
42619: gap of 100 bp
43345: contig of 726 bp
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47449: contig of 7
47549: gap of 10
48287: contig of 7
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44959: contig of
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46635: contig of
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55018: contig of
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54173: contig of
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: gap of
49188: C
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45766: cont
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43345: c
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41689: con
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                  39263: gap of
39983: con
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Best Local Similarity 100.
Matches 116; Conservative
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2 (bases 1 to 2469)
Soderling, S.H., Westphal, R.S. and Scott, J.D.
Direct Submission
Submitted (27-JUL-2000) Howard Hughes Medical Institute/Vollum
Institute, Oregon Health Sciences University, 3181 Sam Jackson Park
Rd., Portland, OR 98201, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /LTGT 11 101-"MPLVKRNIDPRHLCHTALPRGIKNELECVTNISLANITROLSSL
SKYAEDIFGELENEAHSFSFRVNSLQERVDRLSVSVTQLDPKEEELSLQDITHKKAFR
SKTIQDQQLFDRKTLPPLQETYDVCBQPPPLNILTPYRDDGKEGLKFYTNPSVFFDL
MEKMLQDTEDKRKERYQKNILDPREPVPRAFEWQKLAGGPELAEDDA
DLLHKHTADTARANGPASHYETRPQTYVDHMOGSYGLSALPFSQMSELLTRAEBRULVRPH
EPPPPPPMHGAGDAKPTPTCISSATGLIENRPQSPAAGRTPVFVSPTPPPPPPPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-JUL-2000) Genome Sequencing Center, Washington
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Homo sapiens BAC clone RP11-443K8 from 2, complete sequence.
ACO19100
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Pred. No. 1.5e-13;
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Kalicki,J., Drone,K. and Belter,E.
The sequence of Homo sapiens BAC clone RP11-443K8
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1180 caggcagaacacctgtgtttgtgagccccactccccacctcctcc 1225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 40; L. 1.50.13;
100.0%; Pred. No. 1.50.13;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                       /protein_id="AAG02214.1"
/db_xref="G1:9931546"
 19 (17), 4589-4600 (2000)
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Submitted (30-DEC-1999) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates;
1 (bases 1 to 213475)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                        /product="WAVE-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 213475)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO 63108, USA
4 (bases 1 to 213475)
Waterston, R.H.
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Matches 46; Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prepared with primer pairs derived from THC41826; GenBank Accession Numbers-- F10585, T87835, M79145, T06478, T32453, L51665. Location/Qualifiers
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Westphal, R.S., Soderling, S.H., Alto, N.M., Langeberg, L.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2545 actotgacttaaacatacatgtaacttacataactgttaagaataacagtotgatttaat 2604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scar/WAVE-1, a wiskott-aldrich syndrome protein, assembles an actin-associated multi-kinase scaffold
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100.0%; Pred. No. 4.3e-33;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          GenomicDNA: 25 ng
Primer: 0.43 uM each
dNTPs: 230 uM each
AmpliTaq: 0.5 units
TagStart Ab: 0.5 units
Total Volume: 10 ul
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Mus musculus WAVE-1 mRNA, complete cds.
AF290877 GI:9931545
                Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Email: mdadams@tigr.org
                                                                                                                                                                        5min
30sec
                                                                                                                                                                                                                        30sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .225
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .225
                                                                                                                                                                                                          30sec
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                                                                                                Primer A: CTTACACAGTAGACAATATGAAG
Primer B: ACTCTGACTTAAACATACATGTA
STS size: 225
PCR Profile:
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1%
10x
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KCl: 500
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Matches 81; Conservative
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                                                                                                                                                                                                                                                                          Protocol:
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AF290877
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COMMENT
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Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jul 26, 2000 this sequence version replaced 91:7631000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics. Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc :
                                                                                                                                                                         Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 213475)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone RPI1-443K8 contains a transposon which has been omitted from the submitted sequence. The transposon should insert after base position 88497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone sequenced to the right is RP11-465011. Actual start of this clone is at base position 1 of RP11-443K8; actual end is at base position 213475 of RP11-443K8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0443K08
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/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                       Direct Submission
Submitted (10-SEP-2000) Genome
University School of Medicine,
MO 63108, USA
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/rpt_family="Alu"
3343. .3459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          code: WUGSC
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                                                                                                                                                                                                                                                                                                              Waterston, R.
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EST AA402120 (NID:92056976) zt67e01.rl"
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0557, .1004,
                                                                                                                note="similar to
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complement(join(2200. 2567, 2679. 2786, 2884. 2956,
3043. 3119, 3367. 3855, 4103. 4219))
/note="gene_id:MBK20.2"
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LLSCQSWEIMGSFAVDTLDLADLEWSPDDSSIVVWDSPLEYKAYECGLGVKTVSWSPC
GQFLAIGSYDQMLRVLNHLTWKTFAEFLHLSTVRAPCSAAIFKEIDEPLQLDMSELSL
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TRUSAWTALMIWDMRLLEVAAILVQKEPIRANWDPYCTRLLLCTGSSHLYMWTPSG
AFCVCNPLPGFSISDLWMIDGSCLLLKDKDAFCCAPYSLPESSDYSSDD"
COMplement (1914) . 558%, 5725 . 5969)
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TLLHQIAGHIALSLAFDPSRSPHYKVFCLRGRSNNSFSSASDSELYHIEVYSSNFGLW
                   NetGene2 (S.M. Rebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5′ clone is 7211 and the 3′ clone is MXM12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MEFTEAYKQTGPCCFSPNSRYVAVANDYRLVIRDTFSFQVVQLF
SCLDKISYIEWALDSEYILCGLYKKPMIQAWSLTQPEWTCKIDEGPAGISYARWSPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRVVPVPTSPSTFIEFSYSVFWNGAVNWYGFSSRDCLSFDINTQEIKILPLPDHEHED
EPLPDPRIIMFLDESQGNLYYIEVNNQSSSNLRVYEMESNSSSMSVKYNVDLEPLAAA
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http://ccr-081.mit.edu/GENSCAN.html),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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/db_xref="61:9759580"
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/note="gene_id:MBK20.3
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214. .837
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/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                            /strain="Columbia"
  GENSCAN (Chris Burge, MIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene_id:MBK20.1"
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Submitted (07-JNN-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mall:ynakamu@kazusa.or.jp,
Tel:81-438-52-3934,
Address for correspondence: kaos@kazusa.or.jp,
Address for correspondence: kaos@kazusa.or.jp,
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MBK20
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato,S., Kaneko,T., Kotani,H., Nakamura,Y., Asamizu,E., Miyajima,N. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1
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                                                                     /rpt_family="MIR"
31554.31743
.rpt_family="MER1_type"
31791.31900
/rpt_family="MIR"
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                   'rpt_family="MER1_type"
10276. .30528
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34565. 34752
/rpt_family="MIR"
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/rpt_family="ERV1"
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/rpt_family="MaLR"
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13715. .33845
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/rpt_family="MIR"
33120. .33416
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11636 ..11722
/note="gene_1d:MBK20.6"
/forden="tenA-Leu(CAA)"
join(12520. 12539,12693. 12763,12892. .13043,13128. .1324
13356 ..1447,13592. 13681,13826. .13897,14025. .14162,
/note="gplAA7]
gene_1d:MBK20.7
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CTECGYCFCGECRAGHHSGWTCEFYRRESNEPSPEDVER
COMPLEMENT(join(16863. 16984,17088. 17154,17272. 17340,
17462. 17578,17642. 17713,17790. 17884,18056. 18137,
1823. 18282,18422. 18574,18643. 18684,18782. 18880,
18966. 19979,200555. 20122,20745. 20826,20904. 21932,
21053. 21133,21251. 21292,21434. 21532,21630. 21734,
7note="gene_id:MBK20.9"
                                                                                                                                                                                                                                                                                             SLDHNKQGFSSETBELVIFYGGEDLTICDILDAPGEVIGKSSYGTLYKASLQRSGKIR
VERENPVCTVRSDSKEFRATIETLGFRHBRULVPLLGFFAGNGERLAWHPFFGSGN
LSDFIRSGDDESRKMINILATIGTSKALDHLHTGWQKPTVHGNLGSRVVLLSSSFEP
RISDFGLHLLLNLSAGQEILDVSAAEGYKAPELIKMKDVSKESDVYSLGVIMLELVSG
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/codon_start=1
/evidence=not_experimenta1
/protein_id="BABI1441.1"
/db_xref="GI:975584"
/translation="MQFALIPDGPESEENVTRILKVAWVTVPLGIAITIAACIFVLWW
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SLLWQTNWEKVIIFALSQVAXGGSLEPIGYWAYELDGYYRSSNLFPFRGNENDFDN
DLSKWGKLFTFQSFFRKLAPGSLVWRAYFLDFEESSYTIFARFASGDYQEN
KKLGIYLTVAAKLVILIGLIFWAFGPSYSYSLIRLLYGEKWSDGEASLALQFYCLYII
PPEMIRTEYYTDRRIYAFSVIGFVKEETDAASYILLHIPNQAVKYNFIDKTFKKLCDF
                                                                                                                                                                                                                                                                    translation-"MRKSLLLTLLGVSLSAFLIVIFFIIFLRRKESSSTESDQYDVE
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WQILILSSIITLISEKTILDRKNFWETFPLHFGIGVICFCLSAIVIYRRERVFIKRIK
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GAGMWMGFPRPAKKRASLKPLHWVKITSDLQGSLWDELQRRHGDSQTAIELDISELET
LFFVEAKPEKIRLHDLRRASYRVFNVRSYYMRANNKVINLSMPLPDMMTAVLAMDESV
VDVDQIEKLIKFCPTNEEMELLKTYTGDKAALGKYEQYLLELMKVPRLEAKLRVFSFK
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VSDTHTVKSMHYYCKVLASEASELLDVYKDLQSLESASKIQVKSLAQNIQAIIKRLEK
LKQELTASETDGPASEVFCNTLKDFISIAETEMATVLSLYSVVLFKKAHEENVKQADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MCVSTTFWLYCKGLVSEEVIRDESKQIGGFGVAICDHEDNRLYE
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YEHVTSDEKFEVPGCFHRFCFDCIKKQADVALEFAKPVVNCPSFGCNSELQREDCEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(15335. .15610,15690. .16364)
/note="contains similarity to RING zinc finger protein
gene_id:MBK20.8"
                      KSLVNDAPEDHFYRFQRTFQFIKSLANV"
complement(join(7889. .8469,9056. .9554))
/note="contains similarity to receptor-like protein
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/protein_id="BAB11440.1"
/db_xref="G1:9759583"
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/protein_id="BAB11443.1"
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/db_xref="GI:9759585"
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                                                                                                                                  gene_id:MBK20.5"
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from base 100001 (AC073794 Mus musculus clone RP23-
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                     GSAVGFKLKSLLILSDTCAPNSKMTLMHYLCKVLAŠKASDLLDFHKDLESLESAŠKIQ
LKSLABETIQAJTKGLEKLNKQLTASESDGPVSQVFRKVLKDFISMAETQVATVSŠLYS
KLRAFSFKIOFGTOIAELNKGLNAVNSACEEVRTSEKLKEIMANILCMGNILNOGTAE
                                                                        SVGKNADALAHYFGEDPNHYPFEKVTTTLLSFIRLFKKAHEENVKQADLDKNKDAKEA
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Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced 9::8810439.
                                                                                                                     join(23327. .23486,23729. .23834,23917. .24050,24190. ;24
24360. .24446,24519. .24839,25117. .25236,2554. .25658,
25789. .25865,25960. .26035,26117. .26251,26364. .26468,
26640. .26809,26913. .27015,27122. .27234,27523. .27724,
27894. .28025,28107. .2821,28349. .28434,28504. .28599,
28759. .28895,28993. .29095,29179. .29258,29359. .29437,
29528. .20585,29895. .29992,30151. .30245,30343. .30400)
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DOE Joint Genome Institute.
Sequencing of Mouse
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Mus musculus clone RP23-85K13, WORKING DRAFT SEQUENCE, 16 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 78172; 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/product="SMC-like protein"
/protein_id="BABI144.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.3
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24;
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210000
310000
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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Fragment Name Begin
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CNS0707X 993 bp DNA STS 11-JAN-2001
T3 end of clone AZ0AA007E05 of library AZ0AA from strain CBS 712 of
Kluyveromyces marxianus, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (08-SPP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                        Kluyveromyces marxianus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 993)
Llorente, B., Malpertuy, A., Blandin, G., Artiguenave, F., Wincker, P. and Dujon, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Souciet, J. L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Wontigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, Mirkincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic Exploration of the Hemiascomycetous Yeasts: 1. A setrof
yeast species for molecular evolution studies(1)
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic Exploration of the Hemiascomycetous Yeasts: 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kluyveromyčes marxianus var. marxianus
FEBS Lett. 487 (1), 71-75 (2000)
                                                                                                                                                                                                                                                      Kluyveromyces marxianus.
                                                                                                                                                                                              AL423283.1 GI:12206477
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Genoscope.
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                                                     RESULT 15
CNS0707X
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TITLE
JOURNAL
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SOURCE
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                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                Consensus quality: 236727 bases at least Q40
Consensus quality: 24356 bases at least Q30
Consensus quality: 244906 bases at least Q30
Consensus quality: 244906 bases at least Q30
Estimated insert size: 246496; sum-of-contigs estimation
Estimated insert size: 246496; sum-of-contigs estimation
Quality coverage: 7.76 in Q20 bases; agarose-fp estimation

**NOTE: This is a 'working draft' sequence. It currently

* consists of 16 contigs. Gaps between the contigs

* are represented as runs of N The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown length contig of 1522 bp in length gap of unknown length contig of 7047 bp in length gap of unknown length contig of 1513 bp in length contig of 33045 bp in length gap of unknown length gap of unknown length contig of 35085 bp in length gap of unknown length contig of 25089 bp in length
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65394 c 66141 g 57737 t 1504 others
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9 247196: contig of 41678 bp in length.
Location/Qualifiers
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18947: contig of 18947 bp in length
19047: gap of unknown length
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contig of 1328
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gap of unknown
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/db_xref="taxon:10090"
                                                  Web site: http://www.jgi.doe.gov
                                                                                                                                                      Jenter clone name: RPCI-23_85K13
Center: Joint Genome Institute
Center Code: JGI
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This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces thuyveri, Kluyveromyces thermotolerans, Kluyveromyces thermotolerans, Kluyveromyces and saccharomyces hansenii var. lactis, Rluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the extremity of this sequence and for the sequence of the other extremity of this insert.
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Pred. No. 0.89;
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                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4911"
/clone="A20AA007E05"
/clone_lib="A20AA"
/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                        /variety="marxianus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: June 20, 2001, 23:38:51
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Best Local Similarity
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Gaps

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0.9%; Score 24; DB 75; Length 247196; 100.0%; Pred. No. 0.38; tive 0; Mismatches 0; Indels 0;

Db 243129 TCTGGGCTACATCCAACTCCATCT 243106

Qy 1599 tctgggctacatccaactccatct 1622

Query Match 0.99 Best Local Similarity 100.(Matches 24; Conservative

Job time: 19119 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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gb_pr10:*
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67.0 1758
32.8 151580
32.8 192017
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                                                                                 June 20, 2001, 15:04:28; Search time 3470.44 Seconds (without alignments) 11699.624 Million cell updates/sec
                                                                                                                                                                              1 cttctcttgcacttgcggat.....aatggttcattttaaaagtt 2625
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                        1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_htg_other:
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2625
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em_hum7:
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gb_pat2:
gb_ph:*
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gb_ba2:*
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Perfect score:
Sequence:
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Database

Searched:

Run on:

D87459 Human mRNA

Description

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SUMMARIES

Mus musc Homo sap

D87459
AF290877
AF134303
AL590009
AL590549
AC019100
AC021847

278.2 2264.6 2264.6 205.6 205.6 205.6 205.6 205.6 1173.4 1171.8 1186.4 1

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JOURNAL DNA Res 3 (5), 321-329 (1996) MEDLINE 97191544 Location/Qualifiers Location/Qualifiers Location/Qualifiers Ada xref="taxon:9606" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Ha6751" Actione="Rinala" Actione Actio	Duery Match 100.0%; Score 2625; DB 91; Length 2625; Best Local Similarity 100.0%; Pred. No. 0; Matches 2625; Conšervative 0; Mismatches 0; Indels 0; Gaps 1 cttctttgcacttgcggatgatgatgaactggaataacgatgaaagaaa	121 121 181 181 181 241 241 301 361 421 481
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778.2 10.6 1497 85 AB025542 166.4.6 10.1 104597 92 HS393P12 166.4 10.0 1491 89 AF114304 166.5.6 7.8 4450 85 AB020707 173.4 6.6 192019 91 AF00000 91 AF000000 91 AF000000 91 AF000000 91 AF000000 91 AF000000 91 AF000000 91 AF0000000 91 AF000000000000000000000000000000000000	.5 103270 13 .5 196247 13 .5 200542 13 .4 62537 78 .4 75557 93 .3 152081 86	D87459 2625 bp mRNA PRI 10-JUL- D87459.1 GI:1665804 FMTAA0269 B87459.1 GI:1665804 FMTAA0269 FMTAA0269 FMTAA0269 FMANOS sapiens MAGAS SAPIENS M

RESULT 1 D87459 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

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JOURNAL REFERENCE AUTHORS

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ΟY	1681	tgottotgagocaaagogocatocatoaacoctacotgtaatoagtgatgocaggagt
QQ	1681	
γο ς	1741	tgctactggaagcaatacgaaaaggtattcagctacgcaaagtagaagagcagcgtgaac 1800
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QY	2101	ttacagtggcttatctttttttccccctgaaaagactaatttggtcaaataaacca
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RESU AF29 LOCU	LT 0877 S	AF290877 2469 bp mRNA
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Soderling, S. H., Westphal, R.S. and Scott, J.D.
Direct Submission
Submitsed (27-JUL-2000) Howard Hughes Medical Institute/Vollum
Institute, Oregon Health Sciences University, 3181 Sam Jackson Park
Rd., Portland, OR 98201, USA
Location/Qualifiers
J. 2469
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Murinae; Mus
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Westphal,R.S., Soderling,S.H., Alto,N.M., Langeberg,L.K. and
Scott,J.D.
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                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                                                                                             /organism="Mus musculus"
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1. 1680
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Arp2/3 complex activator"
                         Craniata; Vertebrata; E
Sciurognathi; Muridae;
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Pred. No. 0;
1; Mismatches 250; Indels
                                                                  Scar/WAVE-1, a wiskott-aldrich syndrome
extin-associated multi-kinase scaffold
EMBO J. 19 (17), 4589-4600 (2000)
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 2469)
                                                                                                                                                                                                                              /product="WAVE-1"
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86.2%;
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Euteleostomi;

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Craniata; Vertebrata; Catarrhini; Hominidae;

Chordata;

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/function="activates dendritic nucleation of actin
liaments by the Arp2/3 complex"
/note="WASP-family protein: WAVE: similar to Dictyostelium
suppressor of cyclic-AMP receptor"
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Machesky, L.M. and Insall, R.H.
Scarl and the related Wiskott-Aldrich syndrome protein, WAK
regulate the actin cytoskeleton through the Arp2/3 complex
Curr. Biol. 8 (25), 1347-1356 (1998)
                                                                                                                                                                                                                      Machesky, L. M. and Insall, R. H.
Direct Submission
Submitted (12-Mar-1999) Biochemistry, University
Birmingham B15 2TT, England
Location/Qualifiers
                                       1 (bases 1 to 1758)
Bear, J.E., Rawls, J.F. and Saxe, C.L. III.
SCAR, a WASP-related protein, isolated as defects in late Dictyostelium development J. Cell Biol. 142 (5), 1325-1335 (1998)
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Mammalia; Eutheria;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1758; Conservative 0; Mismatches
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cacagottgatocaaaggaagaagaattgtotttgcaagatataacaatgaggaaag 	ttccgaagttctacaattcaagaccagcagcttttcgatcgcaagactttgcctattcc 	ttacaggagacgtacgatgtttgtgaacagcctccacctctcaatatactcactc	agagatgatggtaaggaaggtctgaagttttataccaatccttcgtatttctttgatct 	tggaaagaaaaatgttgcaagatacagaggataagaggaagga	cagaaaaatctagatcgtcctcatgaaccagaaaaagtgccaagagcacctcatgacag 	cggcgagaatggcagaagctggcccaaggtccagagctggctg	ttacataagcatattgaagttgctaatggcccagcctctcattttgaaacaagacctca 	acatacytggatcatatggatcttactcactttctgccttgccatttagtcagat(agtgagcttctgactagagctgaggaaagggtattagtcagaccacatgaaccactcc 	caggagatgcaaaacc 	acaggtttgatagaaaatcgccctcagtcaccagctacaggcagaacacctgtgtttgtc 	agccccactccccactcctccacctcttccatctgccttgtcaacttcctcatta	agagettcaatgaettcaactectecegtecagtaetteceeetecaeetecaeetecage	actgetttgeaagetecageagtaccaccacctecagetectettcagattgeceetgg 	gttetteacecageteeteetecaattgeaceteetagtacageeteetecaecage 	gctagagctgccccagtatgtgagactgtaccagttcatccactcccacaaggtgaagt 	caggggctgcctccaccccaccaccgcctcctctgcctccacctggcattcgaccatc.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 151580) Direct Submission
Submitted (10-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Apr 9, 2001 this sequence version replaced gi:13446548. gettetgagecaaagegecatecateaaceetacetgtaateagtgatgecaggagtgtg 1742 11-APR-2001 bases; sum-of-contigs Quality AL590009.4 GI:13568304 HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces Assembly program: XGAP4; version 4.5 sequencing vector: plasmid; L08752; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 149944 bases at least Q40 consensus quality: 150676 bases at least Q30 consensus quality: 150662 bases at least Q20 insert size: 151080; sum-of-contigs Homo sapiens chromosome 6 clone RP11-181P4, PROGRESS ***, 6 unordered pleces coverage: 6.00x in Q20 bases; agarose-fp Quality coverage: 5.89x in Q20 DNA 151580 bp Center code: SC Homo sapiens AL590009 AL590009 Corby, N. RESULT 4 AL590009/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL 1683 1441 1743 1501 1803 1561 1863 1621 1983 1741 ACCESSION REFERENCE COMMENT g οy qq οy qq δ QQ Qγ q δ q δ g οy g

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Assembly program: XGAP4, version 4.5
Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; LOBY52; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 18717 bases at least Q40
Consensus quality: 188982 bases at least Q20
Consensus quality: 190116 bases at least Q20
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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PROGRESS ***, 11 unordered pieces
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Mammalia; Eutheria; Primates;
1 (bases 1 to 192017)
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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61266. .92318
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92419. .102427
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99.9%;
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100299 ATACTCTGACTTAAACATGTAACTTACATAACTGTTAAGAATAACAGTCTGATTA 100240
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Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Apr 17, 2001 this sequence version replaced gi:13625115.
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*** SEQUENCING IN
                                                                               100719 TTCCCCCTGAAAAGACTAATTTGGTCAAATAAACCACTAAGTATTAAGCATGGACAGCTG
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ttocccctgaaaagactaatttggtcaaataaaccactaagtattaagcatggacagctg
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Catarrhini; Hominidae; Homo
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sum-of-contigs Quality
                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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80484 126461: contig of 45978 bp in length

126462 126561: gap of 100 bp

129108 129207: gap of 100 bp

122208 148782: contig of 19575 bp in length
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4712 4811: gap of 100 bp
4812 15590: contig of 10779 bp in length
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148883 162967: contig of 14085 bp in length
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/note="assembly_fragment:00630
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                                         Quality coverage: 4.85x in Q20 bases; sur
coverage: 4.74x in Q20 bases; agarose-fp
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                     insert size: 195674; agarose-fp
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Db 118245 AGGTATTCAGCTACGCAAAGTAGAAGAGCAGCAGCAACAGGAAGCAAGAGCTAAGCATGAACGCAT 118136
                                                                                                                                                                                                                                                                                                                                          118065 TTACAAAACTGAATGCAAATGTCCTTTGTGGTGCTTGTTCCTTGAAAATGTTTGGTCATT 118006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 118185 TGAAAACGATGTTGCCACCATCCTGTCTCGCCGTATTGCTGTTGAATATAGTGATTCGGA 118126
                                                                                                                                                                                                                                                                                             Db 118125 AGATGATTCAGAATTTGATGAAGTAGATTGGTTGGAGTAAGAAAAATGCATTGATAAATA 118066
                                                                                                                                                                                                                                                                                                                                                                                                                      118005 CTAGTGTTTTGCTTTCTTTTCCTTATAATAATGACCCTTTTCCTCCATAACTTTTGAT 117946
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                                                                                                                                     1763 aggtattcagctacgcaaagtagaagagcagcgtgaacaggaagctaagcatgaacgcat 1822
                                                                                                                                                                                                   1823 tgaaaacgatgttgccaccatcctgtctcgccgtattgctgttgaatatagtgattcgga 1882
                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       ctagtgttttgctttctttccttataataaatgaccctttcctccataacttttgatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                      tctaaggaaaatattagcatacatttcaaactaaatgttttacagtggcttatcttttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  attccatttcctgatgttttaaaagaagaagacactgccttgattatacgaatacactcag
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                                                                           Length 192017;
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              1002 others
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                                                                             DB 82;
                                                                           Score 861.4; DB 82;
Pred. No. 2.4e-163;
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fragment_chain:3"
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Best Local Similarity 99.9%;
Matches 862; Conservative
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

JOURNAL REFERENCE

AUTHORS JOURNAL

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EST AI445193 (NID:94287282) t191h10.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST AA411798 (NID:g2070413) zt67e02.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA402120 (NID:92056976) zt67e01.rl"
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                      libraries. Genomics 51:1-8. The clone may be obtained either irc Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://becpac.med.buffalo.edu)
                                                                                                                                                                            The clone sequenced to the right is RP11-4455011. Actual start of this clone is at base position 1 of RP11-443K8; actual end is at base position 213475 of RP11-443K8.
                                                                                                                                                                                                                                                                          The clone RP11-443K8 contains a transposon which has been omitted from the submitted sequence. The transposon should insert after
       approach for construction of bacterial artificial chromosome
                                                                                                                              VECTOR: PBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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19780. .19865
rpt_family="AcHobo"
1981. .20438
/rpt_family="L2"
20526. .20678
                                                                                                                                                                                                                                                                                              from the submitted sequence.
base position 88497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11"
1525. .1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="MaLR"
10093. 10544
/rpt_family="MaLR"
10557. 10964
/rpt_family="ERVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-443K8"
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alu"
343. 3459
/rpt_family="MIR"
4351. 4676
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="Malk"
1640. .9962
/rpt_family="Malk"
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292. .9531
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note="similar to
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18409. .18912
/note="similar to
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'note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         718. 8054
note="similar to
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rpt_family="Alu"
.7605. .17689
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/rpt_family="L2"
18866. .19002
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rpt_family="Alu"
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19033. .19329
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston.R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jul 26, 2000 this sequence version replaced gi:7631000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this folore. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA 5 (bases 1 to 213475)
Homo sapiens BAC clone RP11-443K8 from 2, complete sequence.
AC019100
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                                                                                                                                                                                                                                                                                              2 (bases 1 to 213475)
Kalicki,J., Drone,K. and Belter,E.
The sequence of Homo sapiens BAC clone RP11-443K8
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                   Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: H_NH0443K08
                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                   1 (bases 1 to 213475)
Sulston, J.E. and Waterston, R.
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                                                     AC019100.4 GI:9454638
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                                                                                                          human.
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL

AUTHORS REFERENCE

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

repeat_region

repeat_region

repeat_region

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved

SOURCE INFORMATION:

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          931
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/rpt_family="MER1_type" 30276. .30528
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24379..24516
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/rpt_family="ERVL"
25975. 27100
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"Type family="Alu"

33715. .3346.

/rpt_family="ERV1"

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34482. .34533
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28156. 28571
/note="similar to
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7216. .27523
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Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Homo sapiens chromosome 6 clone RP11-181P4, WORKING DRAFT SEQUENCE,
32 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                    129638 ATCATTCAAAAAGTACATTTAGCTTGTGTGTTGAACTCTCATAAAGGAATTTTGAATTT 129697
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Jul 7, 2000 this sequence version replaced gi:8567974
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Waterston, R.H.
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Waterston, R.H.
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequenting vector: plasmid; 0% Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 125690 bases at least Q40
Consensus quality: 136641 bases at least Q20
Consensus quality: 13664 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 140712; sum-of-contigs
Quality coverage: 2.84 in Q20 bases; sum-of-contigs
Quality coverage: 3.15 in Q20 bases; sum-of-contigs
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154 109673: contig of 6130 bp.m. length 1674 109673: gap of unknown length 1774 118660: contig of 8887 bp in length 1661 118766: gap of unknown length 1761 130272: contig of 11512 bp in length 1273 130372: gap of unknown length 1773 143812: contig of 13440 bp in length.

Location/Qualifiers
 f unknown length
g of 6404 bp in length
f unknown length
g of 6130 bp in length
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// note="assembly_name:Contig20"
15320. .17854
/note="assembly_name:Contig21"
17955. .20526
/note="assembly_name:Contig22"
20627. .24354
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1917. 4030

note="assembly_name:Contigl4"
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18307. .32673
Anote="assembly_name:Contig25"
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'note="assembly_name:Contig33"
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/note="assembly_name:Contig39"
97040. .103443
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note="assembly_name:Contig35"
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/chromosome="6"
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Identification of two human WAVE/SCAR homologues as general actin regulatory molecules which associate with the Arp2/3 complex Blochem. Blophys. Res. Commun. 260 (1), 296-302 (1999) 99310608
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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181 AACTTCTACATCAGAGCAAATTCTCTTCAAGACAGAATTGATCGCCTTGCTGTCAAAGTC 240
                                                                                                                                                                                                                                         241 ACCCAGCTGGATTCAACAGTGGAAGAGGTCTCACTACAGGATATCAACATGAAAAAAGCT 300
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Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds.
AB026542
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Suetsugu, S., Miki, H. and Takenawa, T.
Direct Submission
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Suetsugu,S., Miki,H. and Takenawa,T.
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/db_xref="taxon:9606"
/cell_type="Jurkat"
/chromosome="X"
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Submitsed (12-APR-1999) to the DDBJ/EWBL/GenBank databases. Shiro
Submitted (12-APR-1999) to the DDBJ/EWBL/GenBank databases. Shiro
Suetsugu, Institute of Medical Science, Unversity of Tokyo,
Department of Blochemistry; 4-6-1, Shirokanedai, Minato-ku, Tokyo
108-8639, Japan (E-mail:suetsugu@ims.u-tokyo.ac.jp,
Tel:+81:3-5449-5508, Fax:+81-3-5449-5417)
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="associates with Arp2/3 complex and regulates actin cytoskeleton"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 ctaagtagcctaagtaaatatgctgaagatatatttggagaattattcaatgaagcacat 422
                                                                                                                                                                                         03-JUL-1999
complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                Suetsugu, S., Miki, H. and Takenawa, T. Identification of two human WAVE/SCAR homologues as general a regulatory molecules which associate with the Arp2/3 complex Biochem. Biophys. Res. Commun. 260 (1), 296-302 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1509;
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Pred. No. 6.9e-47;
0; Mismatches 214;
                                                                                                                                                                                         mRNA
for WASP-family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="WASP-family protein"
/protein_id="BA81796.1"
/db_xref="GI:5263099"
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Direct Submission
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/db_xref="taxon:9606"
/chromosome="13"
                                                                                                                                                                                                                                                                                                                          Homo sapiens brain cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="13q12"
/tissue_type="brain"
1. .1509
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                                               Db 143544 ATAAAGGGGTCATNTAACAGG 143564
                                                                                                                                                                     Homo sapiens WAVE3 mRNA AB026543
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Best Local Similarity
Matches 424; Conserv
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ORIGIN
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2603
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VERSION
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LOCUS
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Shiro

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Proline-rich protein KIAA0269 LIKE
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                                                                                               KYAEDIFGELFTQANTFASRVSSLAERVDRLQVKVTQLDPKEEEVSLQGINTRKAFRS
STIQDQKLFDRNSLPVPVLETYNTCDTPPPLNNLFPYRDDGKEALKFYTDPSYFFDLM
                                                            /db_xref="G1:5257244"
/translation="MPLVTRNIEPRHLCRQTLPSVRSELECVTNITLANVIRQLGSLS
                                                                                                                                             LGTSGYPPTLVYQNGSIGCVENVDASSYPPPPQSDSASSPSPSFSEDNLPPPPAEFSY
PVDNQRGSGLAGPKRSSVVSPSHPPPAPPLGSPPGPKPGFAPPPAPPPPPMIGIPP
                                                                                                                                                                              PPPPVGFGSPGTPPPPSPPPFPPPPPPPPPPPPPPPAADYPTLPPPPLSQPTGGAPP
PPPPPPPPPPPFTGADGQPAIPPPLSDTTKPKSSLPAVSDARSDLLSAIRGGFQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 G---TTAGAAGCGAGCTGGAATGCGTGACCAACATCACCTGGCAAATGTCATCGGCAG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 663 agagatgatggtaaagaaggtctgaagttttataccaatccttcgtatttctttgatcta 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 atgeogetagtgaaaagaaacatogateetaggeaettgtgeeacacageactgeetaga 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 CTGGGCAGCCTGAGTAAATATGCAGAGGACATTTTTGGAGAGCTCTTTACTCAGGCAAAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agtititicciicagagicaactcatigcaagaacgigiggaccgittaictgitagigii 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 GTCTTAGAAAACATACAATACCTGTGATACTCCCCCCTCTCAACAAATCTTACCCCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         538 AAAGAAAAGAAAGATAATCCAAAATCGAGGGAATGTAAAACCCACGTAAAATCAAGACACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 AAGGAAGAGTGGGAGAAATGAAGATGGGGCAAGAATTTGTGGAGTCCAAAGAAAAGCT
                                                                                                                                                                                                             RRVEEQREQEKRDVVGNDVATILSRRIAVEYSDSEDDSSEFDEDDWSD
                                                                                                                                                                                                                                                                                                  Length 1497;
                                                                                                                                                                                                                                                                                               Score 278.2; DB 85; Length
Pred. No. 5.3e-46;
0; Mismatches 228; Indels
             /codon_start=1
/product="WASP-family protein"
/protein_id="BAA81795.1"
actin cytoskeleton"
                                                                                                                                                                                                                               330
                                                                                                                                                                                                                                                                                                10.6%;
64.9%;
                                                                                                                                                                                                                               466 c
                                                                                                                                                                                                                                                                                                                                Matches 428; Conservative
                                                                                                                                                                                                                                                                                                              Local Similarity
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HS393P12 104597 bp DNA PRI 23-NOV-1999 Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical

LOCUS DEFINITION

RESULT 10

HS393P12

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(http://www.sanger.ac.uk/HGP/Chrx/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk IMPORTANT: This sequence is the entire insert of clone 333P12. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre chromosome X mapping group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The true left end of clone 393Pl2 is at 1 in this sequence. The true right end of clone 393Pl2 is at 104597: 393Pl2 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7531. .7631
/note="L1 repeat: matches 12. .111 of consensus"
complement(7750. .8788)
/note="match: cDNAs D16470 U00684 L23868; match: ESTS
H11536 H06620"
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3178. .3565
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                                                                                                                                                     HTG; 60S Ribosomal Protein L7; KIAA0065; KIAA0269; KIAA0412;
KIAA0413; KIAA0569; Zinc Finger.
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/hote="L1 repeat: matches 3840. .2057 of consensus"
6295. .6587
/hote="AluSq repeat: matches 292. .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluSx repeat: matches 1. .297 of consensus"
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                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
gene and a 60S Ribosom
an STS and a GSS (BAC
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                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-APR-1998) Chromosome X Project Group
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                             Contains ESTs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="MLT1F repeat:
                                                       sequence), complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="p11.21"
                                                                                                                        AL022578.1 GI:3080381
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                                L7 LIKE pseudogene.
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/note="Lilyay". 13386
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/note="Lilyay". 14882
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/note="Lilyay repeat: matches 542. .634 of consensus"
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/note="Lilyay repeat: matches 628. .1047 of consensus"
/note="Lilyay repeat: matches 628. .1047 of consensus"
complement(16357. .18188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="dJ393P12.1"
/note="KIAA0413, KIAA0412, KIAA0065, KIAA0569 LIKE Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31944. .32084
/note="MRR42c repeat: matches 839. .984 of consensus"
32130. .3218
/note="MRR42B repeat: matches 889. .1080 of consensus"
32366. .32548
/note="AluJo repeat: matches 302. .128 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MERIA repeat: matches 527. .1 of consensus" 19940. .20017
/note="39 copies of 2 mer 85 % conserved" 21347. .23202 /note="1.1 repeat: matches 1. .1837 of consensus" 23211. .24101 /note="LiPA2 repeat: matches 891. .1 of consensus" 23952. .28452 /note="Li PA2 at the seat: matches 5390. .896 of consensus" 28458. .29225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MER42c repeat: matches 590. .717 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .681 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1 repeat: matches 1828. .4367 of consensus"
11765. .31893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5022 of consensus"
                                                                 .5389 of consensus"
                                                                                                                                                       .179 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="WIR repeat: matches 251. .34 of consensus" (9155. .19691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1 repeat: matches 772. .4 of consensus"
29226. .31770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [6668. 16703

Anote="18 copies of 2 mer 100 % conserved"

16827. 17252

Anote="MSTA repeat: matches 426, .1 of con
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                                                                                                             .896 of
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                                                /note="L1 repeat: matches 4835.
9819. .10714
/note="L1PA14 repeat: matches 3.
12690. .12768
                                                                                                                                                     'note="MIR repeat: matches 258.
12808. .12944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Incomplete repeat."
32569. 32719
70726="L1 repeat: matches 4871."
32728. 32986
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32844. .33425
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33449. .33553
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complement(16357. .18188)
/gene="dJ393P12.1"
16668. .16703
                       repeat: matches
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                                       9424. .9964
/note="L1 rep
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ipt 44094. .48864
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AA432323 AA346214 AA314614 N29922 AA27155 AA8160178
AA32323 AA346244 AA532591 AA344358 AA29175 AA6160178
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AA23239 AA0770509 W44352 AA159062 AA188850
AA58590 H93859 AA070549 AA626822 AA188652 AA188850
AA505589 AA514898 T31400 H81167 AA243245 AA070472 AA58122
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KKKMLQDTRDIMKEKRKHRKEKKDNPNRGNVNPRKIKTRKEEWEKIKMGQEFVESKER
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PPPPIGGGSGCGPPPPESSPSFPPHDDFAAPPLDPPPADYPTLPPPPLAGOTPRGAPP
PPPPIGGGSGCGCGGGGGGAVPPPLSGDTTKPKSSLPAISDLLSAICGGFQLR
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/produci-add39P12.2 (hypothetical Proline-rich protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: protein 092558; match: cDNA D87459; match: ESTs AA618483 AA535513 AA631328 AA461536"
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                                                                                                                                                                                                                                                                      /note="MER44C repeat: matches 728. .217 of consensus"
36651. .36740
                                                                                                                                                                                                            .365 of consensus"
                                                                                                                                              .403 of consensus"
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                                                                                                                                                                                                                                                                                                       /note="MER44A repeat: matches 92. .3 of consensus" 42825. .44318
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63.5%; Pred. No. 4.2e-43;
Live 0; Mismatches 239; Indels
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/note="MSTC repeat: matches 298.
35393. .35752
/note="MLTIA1 repeat: matches 1.
36138. .36651
                             matches 1.
                      'note="MSTD repeat:
14516. .34818
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/gene="dJ393P12.2"</pre>
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1 (Bases 1 to 1491)

Bear, J.E., Rawls, J.F. and Saxe, C.L. III.

SCAR, a WASP-related protein, isolated as a suppressor of receptor defects in late Dictyostelium development

J. Cell Biol. 142 (5), 1325-1335 (1998)
                                                                                                                                                                                                                                                                                       43058 AGTCACTCAGCTGGATCCCAAGGAAGAAGAAGTGTCACTGCAAGTAATCAACACCCGAAA 43117
                                              43118 AGCCTTCAGAAGCTCCACCATTCAAGACCAGAAGCTTTTTGACAGAACTCTCTCCCAGT 43177
                                                                                    CAGGAAAGAAAAGAAAGATAATCCAAATCGAGGGAATGTAAACCCCACGTAAAATCAAGAC 43417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-JUN-1999) Biochemistry, University of Birmingham, Birmingham B15 2TT, England Sequence update by submitter on Jun 14, 1999 this sequence version replaced gi:4927211.

Location/Qualifiers
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                        agctttccgaagttctacaattcaagaccagcagcttttcgatcgcaagactttgcctat
                                                                                                                       ttatagagatgatggtaaagaaggtctgaagttttataccaatccttcgtatttctttga
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                                                                                                                                                                         AF134304 1491 bp DNA PRI
Homo.sapiens Scar2 (SCAR2) gene, partial cds.
AF134304
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/organism="Homo sapiens"

/db_xref="taxon:9606"

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Machesky, L.M. and Insall, R.H.
Direct Submission
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GPFGYPPTLVYQNGSIGCVENVDASSYPPPSQSDSASSPSPSFSEDNLPPPPAEFSYP
VDNQRGSGLAGPKRSSVVSPSHPPPAPPLGSPPSSKPGFAPPPAPPPPPPMIGIPPP
PPPIGEGSPCTPPPPSSSPFPPHPDFRAPPLLPPPPAADYPTLPPPPLSQPTRGAPPP
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PPPPGPGEKWDVAPPLSDTTKPKSSLPAISDAHSDLLSAICQGFQLRR
462 c 319 q 319 t.
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KKMLQDTRDIMKEKRKHRKEKKDNPNRGNVNPRKİKTRKEEWEKİKMGQEFVESKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                        /translation-"PLVTRNIEPRHLCRQTLPSVRSELECVTNITLANVIRQLGSLSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatgatggtaaagaaggtetgaagttttataeceaateettegtatttetttgatetatgg 725
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                            with the Arp2/3 complex"
/note="WASP-family protein; similar to Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cagettgatecaaaggaagaagaattgtetttgeaagatataacaatgaggaaagettte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 262.4; DB 89; Length 1491;
Pred. No. 8.1e-43;
0; Mismatches 236; Indels 3;
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                                                                                   suppressor of cyclic-AMP receptor"
                                                                                                                                                              /protein_id="AAD33053.2"
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                                                                                                                                    /product="Scar2"
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1. .4450
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Primates;
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1. .1368
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                                                                                                                                                                                                     481 ATGGCATATGACAAAGAGCT 500
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Mammalia; Eutheria;
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SYAAGJVPPPPPPQAPEGSQASAPHA
SYAAGJVPPPPPPQAPEGSQASAPHA
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                                                                                                                                                                        a suppressor of receptor
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1369)
Bear, J.E., Rawls, J.F. and Saxe, C.L. III.
SCAR, a WASP-related protein, isolated as a suppressor of recepto: defects in late Dictyostelium development
J. Cell Biol. 142 (5), 1325-1335 (1998)
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                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-MAR-1999) Biochemistry, University of Birmingham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          623
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/note="WASP-family protein; similar to Dictyostelium
suppressor of cyclic-AMP receptor"
   14-JUN-1999
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AF134305 1368 bp mRNA PRI
Homo sapiens Scar3 (KIAA0900) mRNA, partial cds.
AF134305 GI:4927213
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Pred. No. 2.3e-31;
0; Mismatches 174;
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64.6%;
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Matches 323; Conservative
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                                                                                          Homo sapiens
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Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 5 (6), 355-364 (1998)
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SYAAGDVPPHGPASQAAEHEYRPPSASARHMALNRPQQPPPPPPQAPEGSQASAPMA
PADYCHLPAOI I EYYNRSGPPPPPPPPYIPSAGATARYSPLQHPWQPPPASASSTHAA
PPHPPSTGLLVTAPPPPGPPPPPPPPPSISSSSMHGPPVAEAKRQEPAQPISD
ARSDLLAAIRMGIQLKKVQEQRRQEAKREPVGNDVATILSRRIAVEYSDSDDDSEFDE
NDWSD
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/db_xref="G1:4240289"
/tb_xref="G1:4240289"
/tb_xref="G1:4000QV9V5ELFNBANFYIRANSLQDRIDRLAVKVTQLDSTVEEVS
LQDINMKRAFRSSTVQDQQV9V5KNSTPNPVADIYNOSDKPPPLNILTPFRDDKKDGLK
FYTDPSYFFDLWKEKMLQDTEDKRKEKRRQKEQKRIDGTTREVKKVRKARNRRQEWNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-DEC-1998) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII
SK plus clone:hk09606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB020707 4450 bp mRNA PRI 16-JUN-1999,
HOMO Sapiens mRNA for KIAA0900 protein, partial cds.
AB020707
gatacagaggataagaggaaggaaaggaaggaagcagaagcagaaaa---tctagatcgt 800
                                                                  420
                                                                                                                                     801 cctcatgaaccagaaaaagtgccaagagcacctcatgacaggcggcgagaatggcagaag 860
                                             Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
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Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.
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/dev_stage="adult"
/sex="male"
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us-09-425-501-1.rge

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      gctgaagatatatttggagaattattcaatgaagcacatagtttttccttcagagtcaac 443
                                                                                                                                             tcattgcaagaacgtgtggaccgtttatctgttagtgttacacacgcttgatccaaaggaa 503
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                                        Gaps
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Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jul 7, 2000 this sequence version replaced g1:8567974.
                                                                                                                                                                                                                                                                                                                                                           624 tgtgaacagcctccacctctcaatatactcactccttatagagatgatggtaaagaaggt
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                                                                                                                                                                                                                     gaagaattgtcttgcaagatataacaatgaggaaagctttccgaagttctacaattcaa
   Length 4450;
                                       3;
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Score 205.6; DB 85; Length
Pred. No. 2.5e-31;
0; Mismatches 174; Indels
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Homo sapiens chromosome 6
32 unordered pieces.
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Waterston, R.H.
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Waterston, R.H.
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64.68;
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                                   Matches 323; Conservative
                  Similarity
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 Query Match
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ORGANISM
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KEYWORDS
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* NOTE: This is a 'working draft' sequence. It currently
consists of 32 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
      Sequencing vector: plasmid: 0% Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 125690 bases at least Q40 Consensus quality: 130641 bases at least Q30 Consensus quality: 130644 bases at least Q20 Insert size: 151000; agarose-fp Insert size: 140712; sum-of-contigs Quality coverage: 2.84 in Q20 bases; sum-of-contigs Quality coverage: 3.15 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                     contig of 1345 bp in length
gap of unknown length
contig of 1371 bp in length
gap of unknown length
contig of 1314 bp in length
gap of unknown length
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gap of unknown length
contig of 6130 bp in length
gap of unknown length
contig of 8887 bp in length
gap of unknown length
contig of 11512 bp in length
gap of unknown length
gap of unknown length
contig of 13440 bp in length
 bp in length
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note="assembly_name:Contig14"
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note="assembly_name:Contig22"
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note="assembly_name:Contig25"
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1. .143812
contig
gap of
                        contig gap of
                                                                                                                                                                                                                         /clone="RP11-181P4"
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Sims,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     50758 TATTGTTAATTTTTGATTTTCCTACAGGTGAACTGGCACAAAGGTTAATCTCAAGAT 50699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr. 17, 2001 this sequence version replaced gi:13625115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 6 clone RP11-403119, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                       185 tatggctgcaaaatcgttaaaatcttcaaggtgaactggcacaaaggttaatctcaagat 244
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 1008 of reads
Chemistry: Dye-terminator Bub Dye; 1008 of reads
Consensus quality: 187117 bases at least Q40
Consensus quality: 188982 bases at least Q40
Consensus quality: 190116 bases at least Q20
Insert size: 191017; sum-of-contys
Insert size: 195674; agarose-fp
Quality coverage: 4.85x in Q20 bases; sum-of-contigs Quality
coverage: 4.74x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                           Length 143812;
                                                                                                                                                                                                        3122 others
                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                                                                       Similarity 92.0%; Pred. No. 1e-24; 33; Conservative 0; Mismatches 16;
feature 97040. .103443

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109774. .118660
//note="assembly_name:Contig42"
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118761. .130772
//note="assembly_name:Contig43"
118373. .143812
//note="assembly_name:Contig44"
41394 a 27942 c 28670 g 42684 t 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .--- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA403119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL590549.3 GI:13660901
HTG; HTGS_PHASE1.
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Best Local Simi
Matches 183;
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AL590549
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                          15591 15690: gap of 100 bp
15691 80383: contig of 64693 bp in length
                                                                                                                                                                                                                                                                                      80384 80483: gap of 100 bp
80484 126461: contig of 45978 bp in length
                                                                                                                                                                                                                                                                                                                                                                                   np of 100 bp
contig of 19575 bp in length
np of 100 bp
                                                                                                                                                                                                                     10779 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 14085 bp in length
                                                                                                                                                                          1 4711: contig of 4711 bp in length
4712 4811: gap of 100 bp
4812 15590: contig of 10779 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162968 163067: gap of 100 bp

163068 170242: contig of 7175 bp in length

170243 170342: gap of 100 bp

170343 177820: contig of 7478 bp in length

177821 177920: gap of 100 bp

177921 184396: contig of 6476 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177821 177920: gap of 100 bp
177921 184956: contig of 6476 bp in length
184397 184456: gap of 100 bp
184497 192017: contig of 7521 bp in length.
Location/Qualifiers
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fragment_chain:2"

163068. .170242

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fragment_chain:2"

163068. .170242

/ note="assembly_fragment:01301

fragment_chain:2"
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1. .4711
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                                                                                                                                                                                                                                                                                                                                                                                                                              148783 148882; gap of 148883 162967; cont.
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37166 g 58039 t 1002 others

ragment_chain:3 37927 c 37166

57883 a

BASE COUNT ORIGIN

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                                                                                                                                                                           DD 173102 GCGCTAGTGAAAAAAAACATCGATCCTAGGCACTTGTGCCACACAGCACTGCCTAGAGG 173161
                                                                                                                                                                                                                                                 Db 173042 TATTGTTAATTTTTTTTTTTTTCTACAGGTGAACTGGCACAAAGGTTAATCTCAAGAT 173101
                                                                            185 tatggctgcaaaatcgttaaaatcttcaaggtgaactggcacaaaggttaatctcaagat 244
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                                                                                                                                                                                                                                  305 cattaagaatgaactggaatgtgtaaccaatatttccttggcaaatataattagacaact 364
                                         0; Gaps
Score 173.4; DB 82; Length 192017; Pred. No. 1.1e-24; ); Mismatches 16; Indels 0; GZ
                                       ó;
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                                                                                                                                                                                                                                                                                                          aagtagcctaagtaaatat 383
     Query Match 6.6
Best Local Similarity 92.0
Matches 183; Conservative
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